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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:45:11 ; Search time 55 Seconds
(without alignments)
2352.850 Million cell updates/sec

Title: US-10-087-993a-36
Perfect score: 458
Sequence: 1 MSRLSASPLERLEARGG.....NLRIKPKGPPPAEWTRV 458

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	418	91.3	458	2 AAW49908	Aaw49908 Human bra
2	217	47.4	353	7 ADC99051	Adc99051 Human kpp
3	155	33.8	155	2 AAW37255	Aaw37255 Partial h
4	32	7.0	453	2 AAW37254	Aaw37254 Novel non
5	29	6.3	453	2 AAW49906	Aaw49906 Rat prote
6	20	4.4	20	2 AAW71596	Aaw71596 Protein t
7	20	4.4	20	3 AAY81930	Aay81930 Peptide f
8	20	4.4	20	3 AAB08487	Aab08487 Peptide d
9	12	2.6	64	5 ABP07829	Abp07829 Human CRF
10	11	2.4	60	5 ABP04248	Abp04248 Human CRF
11	11	2.4	242	4 AAB59384	Aab59384 Human pro
12	11	2.4	291	4 AAG78282	Aag78282 Human PTP
13	11	2.4	303	5 ABR52340	Abr52340 Protein r
14	11	2.4	692	2 AAY28653	Aay28653 Human Cyt
15	11	2.4	799	4 AAG78623	Aag78623 Human tyr
16	11	2.4	802	2 RAY28654	Ray28654 Murine Cy
17	11	2.4	807	2 AAW89247	Aaw89247 Human PTP
18	11	2.4	808	2 AAY28652	Aay28652 Human Cyt
19	11	2.4	913	2 AAW12522	Aaw12522 Protein t
20	11	2.4	913	2 AAY28156	Aay28156 Human PTP
21	11	2.4	913	5 AAG79333	Aag79333 PIPH1. 8/
22	11	2.4	913	7 ADD22982	Add22982 Human pro
23	10	2.2	20	2 AAW71599	Aaw71599 Protein t
24	10	2.2	20	3 AAY81933	Aay81933 Peptide f
25	10	2.2	20	3 AAB08490	Aab08490 Peptide d

26 10 2.2 31 3 AAY67255 Pro 1 reg
27 10 2.2 31 3 AAY67254 Pro 1 reg
28 10 2.2 127 2 AAW35301 Human pol
29 10 2.2 237 7 ADC64297 Human SID
30 10 2.2 253 4 AAB59383 Human pro
31 10 2.2 296 7 ABM78984 Human leu
32 10 2.2 298 2 AAW35300 Human lel
33 10 2.2 306 4 AAG78268 Human DCA
34 10 2.2 312 4 AAG78281 Human PTP
35 10 2.2 370 2 AAW18093 Type I di
36 10 2.2 376 2 AAW35302 Human lel
37 10 2.2 607 3 AAY81783 Human pro
38 10 2.2 607 3 AAY56098 LAR tyros
39 10 2.2 641 2 AAW35298 Macaque i
40 10 2.2 647 4 AAM23746 Human SST
41 10 2.2 647 4 AAU14379 Human nov
42 10 2.2 723 2 AAW25172 Mouse ins
43 10 2.2 773 5 ABB57374 Mouse lsc
44 10 2.2 775 3 AAY67250 Mouse pro
45 10 2.2 780 3 AAY67252 Human pro

ALIGNMENTS

RESULT 1
AAW49908
ID AAW49908 standard; protein; 458 AA.
XX
AC AAW49908;
XX
DT 20-JUL-1998 (first entry)
XX
DE Human brain derived phosphatase 1 (BDP-1).
XX
KW Brain derived phosphatase 1; BDP-1; human; receptor;
KW protein tyrosine phosphatase; signal transduction; therapy; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9748723-A2.
XX
PD 24-DEC-1997.
XX
PF 17-JUN-1997; 97WO-IB000946.
XX
PR 17-JUN-1996; 96US-0019629P.
PR 09-AUG-1996; 96US-0023485P.
PR 13-NOV-1996; 96US-0030860P.
PR 15-NOV-1996; 96US-0030964P.
PR 19-DEC-1996; 96US-0034286P.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Ullrich A, Kharitonkov AI, Aoki N, Wang HY, Chen Z, Naylor O;
PI Kim YW;
XX
XX WPI; 1998-120302/11.
DR N-PSDB; AAV17099.
XX
PT New phosphatase and kinase enzyme(s) - useful in the diagnosis and
PT treatment of signal transduction disorders.
XX
PS Claim 11; Fig 3a-d; 138pp; English.
XX
CC This polypeptide comprises a novel human protein tyrosine phosphatase
CC (PTP), designated brain derived phosphatase 1 (BDP-1), that is expressed
CC in most tissues and cell lines at basal level, but expressed high in
CC epithelium origin cell lines and cancer cell lines. The amino acid
CC sequence was deduced from a cDNA clone (see AAV17099) isolated from a
CC haematopoietic MEG01 cDNA library. The invention relates to novel
CC proteins (see AAW49906-14) involved in cellular signal transduction and
CC to the nucleic acids (see AAV17097-99) coding for them, and provides

CC vectors, host cells, purified recombinant proteins, methods for
 CC identifying compounds that activate or inhibit the novel proteins, as
 CC well as methods for the diagnosis and treatment of diseases associated
 CC with the novel proteins
 XX Sequence 458 AA;
 SQ
 Query Match 91.3%; Score 418; DB 2; Length 458;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 41 KADGVCSVAGSRPENVRKNRYKDVLPDQTRVLSLLQEGHSDYINGNFIKGVDSLA 100
 DB 41 KADGVCSVAGSRPENVRKNRYKDVLPDQTRVLSLLQEGHSDYINGNFIKGVDSLA 100
 QY 101 YIATOGPLPHLLDFWRLWFEFGVKVILMACREIENGKRCERYWAOEPLQTLFCIT 160
 DB 101 YIATOGPLPHLLDFWRLWFEFGVKVILMACREIENGKRCERYWAOEPLQTLFCIT 160
 QY 161 LIKEKWLNEIMLRTLKVTFOKESRVYQYMSWPDGVPSSPDHMLAWVEEARLQGS 220
 DB 161 LIKEKWLNEIMLRTLKVTFOKESRVYQYMSWPDGVPSSPDHMLAWVEEARLQGS 220
 QY 221 GPEPLCVHCSAGCGRTGVLCTVDYVROLITLQMIIPDFSLFVVLKMKORPAVQTEQ 280
 DB 221 GPEPLCVHCSAGCGRTGVLCTVDYVROLITLQMIIPDFSLFVVLKMKORPAVQTEQ 280
 QY 281 YRFLYHTVAQFCSTLQNASPHYQNIKENCAPLYDDALFRTQALLAIIPRPGGVLSI 340
 DB 281 YRFLYHTVAQFCSTLQNASPHYQNIKENCAPLYDDALFRTQALLAIIPRPGGVLSI 340
 QY 341 SVPGSPGHAMADTVAEQKRGAPAGAGSGTGTGTGARSABEAPLYSKVTTPRAQPGAH 400
 DB 341 SVPGSPGHAMADTVAEQKRGAPAGAGSGTGTGTGARSABEAPLYSKVTTPRAQPGAH 400
 QY 401 AEDARGTLPGRVADQSPAGSGAYEDVAGGAGTGGGFGNLRIGRPGKPRPPAEWTRV 458
 DB 401 AEDARGTLPGRVADQSPAGSGAYEDVAGGAGTGGGFGNLRIGRPGKPRPPAEWTRV 458
 RESULT 2
 ID ADC99051 standard; protein; 353 AA.
 XX
 AC ADC99051;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human KPP protein - SEQ ID 4.
 XX
 KW anti-HIV; anti-allergic; anti-inflammatory; antianaemic; antiparkinsonian;
 KW neutropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
 KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
 KW antidiabetic; nephrotropic; antitumor; thyromimetic; neuroprotective;
 KW osteopathic; antiarthritic; antiparasitic; antihelminthic; antiporiatic;
 KW uropathic; ophthalmologic; antirheumatic; haemostatic; antibacterial;
 KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
 KW cancer; developmental; mental retardation; neurological;
 KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
 KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
 KW helminthic infection; transgenic; gene therapy; human; enzyme.
 XX
 OS Homo sapiens.
 XX
 FN WO200303680-A2.
 XX
 PD 24-APR-2003.
 XX
 PF 17-OCT-2002; 2002WO-US033723.
 XX
 XX 19-OCT-2001; 2001US-0345474P.
 FR
 FR 02-NOV-2001; 2001US-0343910P.

PR 13-NOV-2001; 2001US-0333098P.
 PR 16-NOV-2001; 2001US-0332424P.
 PR 30-NOV-2001; 2001US-0334288P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX
 XX Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
 PI Emerling EM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
 PI Gururajan R, Hafalia AJA, Khan FA, Lal PG, Lee EA, Lee SY;
 PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
 PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
 PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
 PI Zebbarjadian Y;
 XX
 XX WPI: 2003-403214/38.
 DR N-PSDB; ADC99103.
 XX
 XX New human kinases and phosphatases and polynucleotides, useful for
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
 PT cancer or hepatitis.
 XX
 XX Claim 1; SEQ ID NO 4; 424pp; English.
 XX
 XX The invention relates to a novel isolated polypeptide which is a human
 CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
 CC agonists and antagonists are useful for diagnosing, treating or
 CC preventing cell proliferative disorders such as atherosclerosis,
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
 CC retardation, neurological disorders including Alzheimer's disease and
 CC Parkinson's disease, autoimmune and inflammatory disorders such as
 CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the
 CC polynucleotides encoding KPP may be useful for creating transgenic
 CC animals to model human disease, as well as during gene therapy
 CC procedures. The current sequence is that of the human KPP protein of the
 CC invention.
 XX
 XX Sequence 353 AA;
 SQ
 Query Match 47.4%; Score 217; DB 7; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.5e-203;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 139 KRCERYWAOEPLQTLGFCITLKEKWLNEIMLRTLKVTFOKESRVYQYMSWPD 198
 DB 32 KRCERYWAOEPLQTLGFCITLKEKWLNEIMLRTLKVTFOKESRVYQYMSWPD 91
 QY 199 GVPSSPDHMLAWVEEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVROLITLQMIIPDF 258
 DB 92 GVPSSPDHMLAWVEEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVROLITLQMIIPDF 151
 QY 259 SLFDVVLKMKORPAVQTEQYRFLYHTVAQFCSTLQNASPHYQNIKENCAPLYDDAL 318
 DB 152 SLFDVVLKMKORPAVQTEQYRFLYHTVAQFCSTLQNASPHYQNIKENCAPLYDDAL 211
 QY 319 FLRTPOALLAIIPRPGGVLSISVPGSPGHAMADTYA 355
 DB 212 FLRTPOALLAIIPRPGGVLSISVPGSPGHAMADTYA 248
 RESULT 3
 AAW37255
 ID AAW37255 standard; protein; 155 AA.
 XX
 AC AAW37255;
 XX
 DT 09-APR-1998 (first entry)
 XX
 DE Partial human non-receptor tyrosine phosphatase.
 XX
 KW Non-receptor protein tyrosine phosphatase; hematopoietic stem cell;
 KW PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist;

KW tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist;
 KW stem cell differentiation.
 XX Homo sapiens.
 OS WO9735019-A1.
 XX 25-SEP-1997.
 XX 17-MAR-1997; 97WO-US005278.
 XX 22-MAR-1996; 96US-00620526.
 XX (GETH) GENENTECH INC.
 XX Lasky LA, Cheng J;
 XX WPI; 1997-480224/44.
 DR N-PSDB; AAV03128.
 XX Haematopoietic stem cell non-receptor protein tyrosine phosphatase -
 PT useful for expansion of undifferentiated stem cells in cell culture.
 XX Claim 9; Fig 8; 66pp; English.

XX The present sequence represents a partial human non-receptor protein
 CC tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein
 CC is predominantly expressed in early hematopoietic stem cells (HSCs) or
 CC progenitor cells, and lacks expression in adult tissues. The protein has
 CC a N-terminal tyrosine phosphatase domain, followed by a region rich in
 CC serine, threonine and proline and a C-terminal region of about 15-25
 CC amino acids which is rich in basic amino acid residues. The protein is
 CC capable of tyrosine dephosphorylation in hematopoietic progenitor cells,
 CC and functional derivatives of such native tyrosine phosphatases. The
 CC phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or
 CC progenitor cell can be used in an assay for the identification of PTP HSC
 CC antagonists or agonists. The antagonist can be used to induce the
 CC differentiation of stem cells, such as undifferentiated malignant
 CC hematopoietic cells, e.g. leukaemia cells, which may facilitate their
 CC treatment. The PTP HSC or an agonist antibody against the PTP HSC can be
 CC used for the expansion of undifferentiated stem cells in cell culture
 CC (this allows expansion of HSC prior to autologous or heterologous bone
 CC marrow transplantation), while the agonist antibody along with a
 CC hematopoietic growth factor can be used for the expansion of
 CC undifferentiated stem cells in vivo

SQ Sequence 155 AA;
 Query Match 33.8%; Score 155; DB 2; Length 155;
 Best Local Similarity 100.0%; Pred. No. 3.9e-143;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 ARGREGAVLAGFSDIQASAAKADGVCSWAGSRPENVRKRYKDVLPYDQTRVILS 76
 DB 1 ARGREGAVLAGFSDIQASAAKADGVCSWAGSRPENVRKRYKDVLPYDQTRVILS 60
 QY 77 LLOBEGHSDYNGFIRGVDSLAYATQGPLPHTLLDFWRLVWVFGVKVILMACREIN 136
 DB 61 LLOBEGHSDYNGFIRGVDSLAYATQGPLPHTLLDFWRLVWVFGVKVILMACREIN 120
 QY 137 GRKRCERYWAQEPLOTGLFCITLIKEKWLNEDI 171
 DB 121 GRKRCERYWAQEPLOTGLFCITLIKEKWLNEDI 155

RESULT 4
 AAW37254
 ID AAW37254 standard; protein; 453 AA.
 XX
 AC AAW37254;
 XX 09-APR-1998 (first entry)
 DT
 XX

DE Novel non-receptor tyrosine phosphatase of hematopoietic stem cells.
 XX
 KW Non-receptor protein tyrosine phosphatase; hematopoietic stem cell;
 KW PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist;
 KW tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist;
 KW stem cell differentiation.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FH Domain 6..303
 FT /note= "tyrosine phosphatase domain"
 FT Active-site 37
 FT /note= "phosphorylated by protein kinases A and C; also
 FT appears to negatively regulate PTPase activity"
 FT Active-site 229
 FT /note= "active site cysteine residue"
 FT Region 312..428
 FT /note= "Pro, Ser and Thr rich region"
 FT Region 430..450
 FT /note= "homologous to a nuclear localization signal found
 FT on murine PTP PEP"
 XX
 PN WO9735019-A1.
 XX 25-SEP-1997.
 XX 17-MAR-1997; 97WO-US005278.
 XX 22-MAR-1996; 96US-00620526.
 XX (GETH) GENENTECH INC.
 XX Lasky LA, Cheng J;
 XX WPI; 1997-480224/44.
 DR N-PSDB; AAV03112.
 XX Haematopoietic stem cell non-receptor protein tyrosine phosphatase -
 PT useful for expansion of undifferentiated stem cells in cell culture.
 XX Claim 9; Fig 1; 66pp; English.

XX The present sequence represents a novel murine non-receptor protein
 CC tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein
 CC is predominantly expressed in early hematopoietic stem cells (HSCs) or
 CC progenitor cells, and lacks expression in adult tissues. The protein has
 CC a N-terminal tyrosine phosphatase domain, followed by a region rich in
 CC serine, threonine and proline and a C-terminal region of about 15-25
 CC amino acids which is rich in basic amino acid residues. The protein is
 CC capable of tyrosine dephosphorylation in hematopoietic progenitor cells,
 CC and functional derivatives of such native tyrosine phosphatases. The
 CC phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or
 CC progenitor cell can be used in an assay for the identification of PTP HSC
 CC antagonists or agonists. The antagonist can be used to induce the
 CC differentiation of stem cells, such as undifferentiated malignant
 CC hematopoietic cells, e.g. leukaemia cells, which may facilitate their
 CC treatment. The PTP HSC or an agonist antibody against the PTP HSC can be
 CC used for the expansion of undifferentiated stem cells in cell culture
 CC (this allows expansion of HSC prior to autologous or heterologous bone
 CC marrow transplantation), while the agonist antibody along with a
 CC hematopoietic growth factor can be used for the expansion of
 CC undifferentiated stem cells in vivo

SQ Sequence 453 AA;
 Query Match 7.0%; Score 32; DB 2; Length 453;
 Best Local Similarity 100.0%; Pred. No. 3.1e-22;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 100 AYIATQGPLPHTLLDFWRLVWVFGVKVILMAC 131
 DB 100 AYIATQGPLPHTLLDFWRLVWVFGVKVILMAC 131

PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.
XX
XX Disclosure; SEQ ID NO 15640; 1037pp; English.
XX
XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, diabetes mellitus, systemic
CC transplantation, cardiovascular diseases, disorders related to organ
CC storage disease, various immune deficiencies and disorders, rheumatoid
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 64 AA;

Query Match 2.6%; Score 12; DB 5; Length 64;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCAGCGRTGV 238
Db | | | | | | | | | |
7 VHCAGCGRTGV 18

RESULT 10
ABP04248
ID ABP04248 standard; protein; 60 AA.
XX
XX ABP04248;
XX
XX 25-JUN-2002 (first entry)
XX
XX Human ORFX protein sequence SEQ ID NO:8478.
XX
XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.
XX
XX Homo sapiens.
XX
XX WO200192523-A2.
XX
XX 06-DEC-2001.
XX
XX 29-MAY-2001; 2001WO-US010836.
XX
XX 30-MAY-2000; 2000US-0206132P.
XX
XX 29-AUG-2000; 2000US-0228716P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX PA

XX Shimkets RA, Leach MD;
XX WPI; 2002-106308/14.
XX N-PSDB; ABN20000.
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing,
XX preventing and treating cardiovascular disease, neurodegenerative,
XX hyperproliferative disorders and autoimmune disorders.
XX
XX Disclosure; SEQ ID NO 8478; 1037pp; English.
XX
XX The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, diabetes mellitus, systemic
CC transplantation, cardiovascular diseases, disorders related to organ
CC storage disease, various immune deficiencies and disorders, rheumatoid
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 60 AA;

Query Match 2.4%; Score 11; DB 5; Length 60;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 KNRVKDVLPLD 69
Db | | | | | | | | | |
7 KNRVKDVLPLD 17

RESULT 11
AAB59384
ID AAB59384 standard; protein; 242 AA.
XX
XX AAB59384;
XX
XX 21-MAR-2001 (first entry)
XX
XX Human protein tyrosine phosphatase #15.
XX
XX Protein tyrosine phosphatase; human; mouse; fruit fly; PTP;
KW substrate trapping.
XX
XX Homo sapiens.
XX
XX WO200075339-A1.
XX
XX 14-DEC-2000.
XX
XX 24-MAY-2000; 2000WO-US014211.
XX
XX 03-JUN-1999; 99US-0137319P.
XX
XX 16-JUN-1999; 99US-00334575.
XX
XX (COLD-) COLD SPRING HARBOR LAB.
XX
XX PA

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VHCAGCGRTG 237
 |||||
 Db 225 VHCAGCGRTG 235

RESULT 14
 AAY28653
 ID AAY28653 standard; protein; 692 AA.
 XX
 AC AAY28653;
 XX
 DT 01-OCT-1999 (first entry)
 XX
 DE Human Cytoplasmic phosphatase, Lyp2 protein.
 XX
 KW Lymphoid Protein Tyrosine Phosphatase; Lyp protein; immunosuppressant;
 KW intracellular tyrosine phosphatase; PTPase; fetal liver, transplant;
 KW resting lymphoid cell; protein tyrosine kinase; PTKs; lymphocyte;
 KW T cell antigen receptor signalling; cytokine receptor signalling;
 KW autoimmune disease; intronic sequence; alternative mRNA splicing.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 27..289
 FT /label= PTPase domain
 FT /note= "Single catalytic protein tyrosine phosphatase
 FT domain"
 FT Domain 469..472
 FT /label= NXY motif
 FT /note= "Unique sequence recognised by phosphotyrosine
 FT binding (PTB) domain"
 FT Binding-site 615..623
 FT /label= SH3 binding site
 FT /note= "Proline rich sequence"
 XX
 PN WO9936548-A1.
 XX
 PD 22-JUL-1999.
 XX
 PF 18-JAN-1999; 99WO-CA000038.
 XX
 PR 16-JAN-1998; 98CA-02220853.
 XX
 PA (HSCR-) HSC RES & DEV LP.
 XX
 PI Roifman CW;
 XX
 DR WPI; 1999-444404/37.
 XX
 DR N-PSDB; AAX90696.
 XX
 PT New nucleic acid encoding intracellular tyrosine phosphatase and related
 PT proteins, used to modulate signaling through T cells, particularly as
 PT immunosuppressant.
 XX
 PS Claim 4b; Page 55; 105pp; English.
 XX

The present protein sequence is that of the cytoplasmic, Lymphoid Protein
 Tyrosine Phosphatase, Lyp2 protein that has a single catalytic domain.
 The non-catalytic portion of the phosphatase contains unique sequences,
 including a single PEST sequence rich in Pro, Glu or Asp, Ser and Thr. It
 is expressed significantly in fetal liver and in resting lymphoid cells.
 Lyp2 is an isoform of the Lyp1 gene that arises by alternative splicing
 of the mRNA. The intronic sequence of Lyp1 encodes for the C-terminal 7
 aminoacids and part of the 3'untranslated region of Lyp2. Lyp2 shares
 sequence identity with the murine phosphatase Z70PEP. Lyp proteins are
 important for regulation of T cell antigen and cytokine receptor
 signalling and for early and late stages of T cell differentiation. Lyp2
 has immunosuppressive activity. Compounds that increase expression of Lyp
 protein can be used as immunosuppressive agents to reduce or prevent T
 cell activation or proliferation, to control thymocyte differentiation,

CC to treat autoimmune diseases and transplant situations
 XX
 SQ Sequence 692 AA;
 Query Match 2.4%; Score 11; DB 2; Length 692;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 228 HCSAGCGRTGV 238
 |||||
 Db 226 HCSAGCGRTGV 236

RESULT 15
 AAG78623
 ID AAG78623 standard; protein; 799 AA.
 XX
 AC AAG78623;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Human tyrosine phosphatase.
 XX
 KW Human; tyrosine phosphatase; hPTP.
 XX
 OS Homo sapiens.
 XX
 PN CN1302899-A.
 XX
 PD 11-JUL-2001.
 XX
 PF 29-OCT-1999; 99CN-00119935.
 XX
 PR 29-OCT-1999; 99CN-00119935.
 XX
 PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
 XX
 PI Ren S, Wu T, Qian B;
 XX
 DR WPI; 2001-550591/62.
 DR N-PSDB; AAX79342.
 XX
 PT Human protein tyrosine phosphatase and its coding sequence.
 XX
 PS Claim 4; Page 12-13 (Disclosure); 29pp; Chinese.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC tyrosine phosphatase hPTP. The protein is expressed in human normal
 CC suprarenal tissue. The present sequence is the protein of the invention
 XX
 SQ Sequence 799 AA;
 Query Match 2.4%; Score 11; DB 4; Length 799;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 228 HCSAGCGRTGV 238
 |||||
 Db 226 HCSAGCGRTGV 236

Search completed: August 17, 2004, 20:51:35
 Job time : 57 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:50:37 ; Search time 20 Seconds
(without alignments)
1182.235 Million cell updates/sec

Title: US-10-087-993A-36
Perfect score: 458
Sequence: 1 MSRLSARSFLERLARGG.....NLRGPKGRPPAETWTRV 458

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	33.8	155	3	US-08-821-278A-17
2	32	7.0	453	3	US-08-821-278A-2
3	29	6.3	453	3	US-08-951-260A-7
4	29	6.3	453	4	US-09-430-626A-7
5	20	4.4	20	3	US-08-938-830-20
6	20	4.4	20	3	US-09-020-222-20
7	11	2.4	231	2	US-08-446-345-37
8	11	2.4	242	2	US-08-685-922-21
9	11	2.4	242	2	US-09-144-925-21
10	11	2.4	244	4	US-09-848-294-7
11	11	2.4	278	3	US-08-821-278A-18
12	11	2.4	802	3	US-09-081-345-18
13	11	2.4	807	3	US-09-081-345-2
14	11	2.4	913	4	US-08-848-294-2
15	10	2.2	20	3	US-08-938-830-23
16	10	2.2	20	3	US-09-020-222-23
17	10	2.2	127	4	US-08-811-481-5
18	10	2.2	127	4	US-09-876-527-5
19	10	2.2	246	4	US-08-884-569A-3
20	10	2.2	250	2	US-08-685-992-7
21	10	2.2	250	2	US-09-144-925-7
22	10	2.2	253	2	US-08-685-992-20
23	10	2.2	253	2	US-09-144-925-20
24	10	2.2	272	3	US-08-821-278A-19
25	10	2.2	289	1	US-08-036-210-13
26	10	2.2	289	2	US-08-449-609-13
27	10	2.2	289	4	US-09-361-096A-13

28 10 2.2 298 4 US-08-811-481-4 Sequence 4, Appli
29 10 2.2 298 4 US-08-876-527-4 Sequence 4, Appli
30 10 2.2 376 4 US-08-811-481-7 Sequence 7, Appli
31 10 2.2 376 4 US-08-876-527-7 Sequence 7, Appli
32 10 2.2 641 4 US-08-811-481-2 Sequence 2, Appli
33 10 2.2 641 4 US-08-876-527-2 Sequence 2, Appli
34 10 2.2 723 2 US-08-548-159-5 Sequence 5, Appli
35 10 2.2 818 4 US-08-811-481-22 Sequence 22, Appli
36 10 2.2 818 4 US-08-876-527-22 Sequence 22, Appli
37 10 2.2 969 2 US-08-548-159-1 Sequence 1, Appli
38 10 2.2 986 2 US-08-548-159-3 Sequence 3, Appli
39 10 2.2 1001 4 US-08-884-569A-2 Sequence 2, Appli
40 10 2.2 1012 4 US-08-811-481-16 Sequence 16, Appli
41 10 2.2 1012 4 US-08-876-527-16 Sequence 16, Appli
42 10 2.2 1501 2 US-08-447-454-3 Sequence 3, Appli
43 10 2.2 1501 2 US-08-716-679-3 Sequence 3, Appli
44 10 2.2 1911 1 US-08-348-006B-5 Sequence 5, Appli
45 10 2.2 1911 2 US-08-800-825A-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-821-278A-17
; Sequence 17, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 17
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo Sapien
US-08-821-278A-17

Query Match 33.8%; Score 155; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.9e-134; Indels 0; Gaps 0;
Matches 155; Conservative 0; Mismatches 0

QY 17 ARGREGAVLAGEFSDIQACSAANKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS 76
Db 1 ARGREGAVLAGEFSDIQACSAANKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS 60
QY 77 LQEGHSDYINGNFIKRGVDSGLAVIATCGPLPHTLLDFWRLVWFEFGVKVILMACREIEN 136
Db 61 LQEGHSDYINGNFIKRGVDSGLAVIATCGPLPHTLLDFWRLVWFEFGVKVILMACREIEN 120
QY 137 GRKRCERYWAQOEPIQTGLFCITLILKEKWLNEDI 171
Db 121 GRKRCERYWAQOEPIQTGLFCITLILKEKWLNEDI 155

RESULT 2
US-08-821-278A-2
; Sequence 2, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 2
; LENGTH: 453
; TYPE: PRT

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; ORGANISM: Mus Musculus
US-08-821-278A-2

Query Match          7.0%; Score 32; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 4.1e-21;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AYIATQPLPHTLLDFWRLVWFGVKVILMAC 131
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Db 100 AYIATQPLPHTLLDFWRLVWFGVKVILMAC 131

RESULT 3
US-08-951-260A-7
; Sequence 7, Application US/08951260A
; Patent No. 6004791
; GENERAL INFORMATION:
; APPLICANT: Aoki, Naohito
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
; AND RELATED PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,260A
; FILING DATE: October 16, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,860
; FILING DATE: June 17, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 227/004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-951-260A-7

Query Match          6.3%; Score 29; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 GAQTGGGLGNLRIGRPKGPDPPEWTRV 458
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Db 425 GAQTGGGLGNLRIGRPKGPDPPEWTRV 453

RESULT 4
US-09-430-626A-7

Query Match          6.3%; Score 29; DB 3; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 GAQTGGGLGNLRIGRPKGPDPPEWTRV 458
    |||||
Db 425 GAQTGGGLGNLRIGRPKGPDPPEWTRV 453

RESULT 5
US-08-938-830-20
; Sequence 20, Application US/08938830
; Patent No. 6040437
; GENERAL INFORMATION:
; APPLICANT: Lasky, Laurence A.
; APPLICANT: Dowbenko, Donald J.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
; AND RELATED PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
```

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; Sequence 7, Application US/09430626A
; Patent No. 6482605
; GENERAL INFORMATION:
; APPLICANT: Aoki, Naohito
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
; AND RELATED PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,626A
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/951,260
; FILING DATE: October 16, 1997
; APPLICATION NUMBER: 60/030,860
; FILING DATE: No. 6482605ember 13, 1996
; APPLICATION NUMBER: PCT/1897/00946
; FILING DATE: June 17, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 227/004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-430-626A-7

Query Match          6.3%; Score 29; DB 4; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.3e-18;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 GAQTGGGLGNLRIGRPKGPDPPEWTRV 458
    |||||
Db 425 GAQTGGGLGNLRIGRPKGPDPPEWTRV 453

RESULT 5
US-08-938-830-20
; Sequence 20, Application US/08938830
; Patent No. 6040437
; GENERAL INFORMATION:
; APPLICANT: Lasky, Laurence A.
; APPLICANT: Dowbenko, Donald J.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
; AND RELATED PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
```

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; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,830
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/798419
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1066P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-938-830-20
;
; Query Match 4.4%; Score 20; DB 3; Length 20;
; Best Local Similarity 100.0%; Pred. No. 2.5e-11;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 437 GFNLRIGRPKGPRDPPAEWT 456
; DB 1 GFNLRIGRPKGPRDPPAEWT 20
;
; RESULT 6
; US-09-020-222-20
; Sequence 20, Application US/09020222
; Patent No. 6111073
; GENERAL INFORMATION:
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
; TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPS)
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,222
; FILING DATE: 06-Feb-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/798419
; FILING DATE: 02/07/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1066t1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
;
; QY 437 GFNLRIGRPKGPRDPPAEWT 456
; DB 1 GFNLRIGRPKGPRDPPAEWT 20
;
; RESULT 7
; US-08-446-345-37
; Sequence 37, Application US/08446345
; Patent No. 5831089
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Moller, Niels P.H.
; APPLICANT: Moller, Karin B.
; TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASES PTP-D1
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,345
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,440
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30742
; REFERENCE/DOCKET NUMBER: 7683-054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-446-345-37
;
; Query Match 2.4%; Score 11; DB 2; Length 231;
; Best Local Similarity 100.0%; Pred. No. 0.042;
; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 59 KRYKQVLPLVD 69
; DB 4 KRYKQVLPLVD 14
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RESULT 8
US-08-685-992-21
; Sequence 21, Application US/08685992
; Patent No. 5912138
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,992
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-685-992-21
Query Match 2.4%; Score 11; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KNRKDVLPYD 69
Db 15 KNRKDVLPYD 25

RESULT 9
US-09-144-925-21
; Sequence 21, Application US/09144925
; Patent No. 5951979
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02421-4799
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,925
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/685,992
; FILING DATE: July 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-144-925-21
Query Match 2.4%; Score 11; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KNRKDVLPYD 69
Db 15 KNRKDVLPYD 25

RESULT 10
US-09-848-294-7
; Sequence 7, Application US/09948294
; Patent No. 6479640
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: Isolation of A CDNA Encoding A No. 6479640el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; TITLE OF INVENTION: Adhesions and Uses Therefor
; FILE REFERENCE: CSHL90-04FZA
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/235,251
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 07/494,036
; PRIOR FILING DATE: 1990-03-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-7
Query Match 2.4%; Score 11; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KNRKDVLPYD 69
|||||
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Db      4 KIRYKDVLPYD 14

RESULT 11
US-08-821-278A-18
; Sequence 18, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821.278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-08-821-278A-18

Query Match      2.4%; Score 11; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      228 HCSAGCGRTGV 238
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Db      203 HCSAGCGRTGV 213

RESULT 12
US-09-081-345-18
; Sequence 18, Application US/09081345
; Patent No. 6228641
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; APPLICANT: Gregory D. Plowman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: PTP04 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,345
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/047,222
; FILING DATE: May 20, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/253
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 802 amino acids
; TYPE: amino acid

Db      228 HCSAGCGRTGV 238
      |||||
Db      203 HCSAGCGRTGV 213

RESULT 13
US-09-081-345-2
; Sequence 2, Application US/09081345
; Patent No. 6228641
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; APPLICANT: Gregory D. Plowman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: PTP04 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,345
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/047,222
; FILING DATE: May 20, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/253
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-081-345-2

Query Match      2.4%; Score 11; DB 3; Length 807;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      228 HCSAGCGRTGV 238
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Db      226 HCSAGCGRTGV 236

RESULT 14
US-09-848-294-2
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-081-345-18

Query Match      2.4%; Score 11; DB 3; Length 802;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      228 HCSAGCGRTGV 238
      |||||
Db      226 HCSAGCGRTGV 236

RESULT 13
US-09-081-345-2
; Sequence 2, Application US/09081345
; Patent No. 6228641
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; APPLICANT: Gregory D. Plowman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: PTP04 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,345
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/047,222
; FILING DATE: May 20, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/253
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-081-345-2

Query Match      2.4%; Score 11; DB 3; Length 807;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      228 HCSAGCGRTGV 238
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Db      226 HCSAGCGRTGV 236

RESULT 14
US-09-848-294-2
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; Sequence 2, Application US/09848294
; Patent No. 6479640
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; TITLE OF INVENTION: Adhesions and Uses therefor
; FILE REFERENCE: CSHL90-04FZA
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/235,251
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 07/494,036
; PRIOR FILING DATE: 1990-03-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 913
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-2

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Query Match 2.4%; Score 11; DB 4; Length 913;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 59 KNRYKDVLPYD 69
Db 673 KNRYKDVLPYD 693

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RESULT 15

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US-08-938-830-23
; Sequence 23, Application US/08938830
; Patent No. 6040437
; GENERAL INFORMATION:
; APPLICANT: Lasky, Laurence A.
; APPLICANT: Dowbenko, Donald J.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
; TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPs)
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,830
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/798419
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Drager, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: F1066P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881

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; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-938-830-23

Query Match 2.2%; Score 10; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 334 GGVLRISISVP 343
Db 1 GGVLRISISVP 10

Search completed: August 17, 2004, 20:56:37
Job time : 21 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 17, 2004, 20:52:38 ; Search time 46 Seconds
(without alignments)

3125.622 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 458

Sequence: 1 MSRLSDARSFLERLEARGG.....NLRIGRPKGRDPPAEWTRV 458

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1292805 seqs, 313927144 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
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15: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	458	100.0	458	13	US-10-087-993-36
2	29	6.3	453	14	US-10-243-687-7
3	24	5.2	448	13	US-10-087-993-32
4	20	4.4	20	14	US-10-340-288-13
5	12	2.6	750	9	US-09-801-368-280
6	12	2.6	750	15	US-10-369-493-22392
7	11	2.4	235	12	US-10-087-684-94
8	11	2.4	235	12	US-10-218-779-94
9	11	2.4	235	12	US-10-072-012-819
10	11	2.4	244	9	US-09-848-294-7
11	11	2.4	244	14	US-10-293-231-7
12	11	2.4	263	12	US-10-087-684-93
13	11	2.4	263	12	US-10-218-779-93
14	11	2.4	291	9	US-09-788-626-22
15	11	2.4	692	15	US-10-309-423-4

Sequence 40, Appl
Sequence 18, Appl
Sequence 55, Appl
Sequence 5, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 38, Appl
Sequence 282, App
Sequence 1750, Ap
Sequence 5, Appl
Sequence 5, Appl
Sequence 13, Appl
Sequence 3, Appl
Sequence 9, Appl
Sequence 4, Appl
Sequence 8, Appl
Sequence 21, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 722, App
Sequence 845, App
Sequence 75, Appl
Sequence 848, App
Sequence 69, Appl

703 15 US-10-366-547-40
802 9 US-09-822-295-18
802 15 US-10-366-547-95
802 15 US-10-309-423-5
807 9 US-09-822-295-2
808 15 US-10-309-423-2
913 9 US-09-848-294-2
913 14 US-10-293-231-2
913 15 US-10-366-547-38
928 9 US-09-801-368-282
928 15 US-10-369-493-1750
127 9 US-09-878-527-5
127 14 US-10-124-089-5
289 14 US-10-314-232-13
296 14 US-10-374-539-3
296 15 US-10-374-499-9
298 9 US-09-876-527-4
298 14 US-10-124-089-4
306 9 US-09-788-626-8
312 9 US-09-788-626-21
376 9 US-09-876-527-7
376 14 US-10-124-089-7
382 15 US-10-366-547-77
641 9 US-09-876-527-2
641 14 US-10-124-089-2
647 15 US-10-291-265-722
773 16 US-10-322-281-845
775 15 US-10-366-547-75
778 16 US-10-322-281-848
780 15 US-10-366-547-69

ALIGNMENTS

RESULT 1

US-10-087-993-36
; Sequence 36, Application US/10087993
; Publication No. US20020169303A1

GENERAL INFORMATION:

APPLICANT: Ullrich, Axel
Aoki, Naohito
Kim, Yeong Woong
Wang, Hong Yang
Chen, Zhengjun
Naylor, Oliver
Kharitonov, Alexei Igorevich
AND SIRP POLYPEPTIDES AND RELATED
PRODUCTS AND METHODS

NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/087,993
FILING DATE: 05-Mar-2002
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/877,150
FILING DATE: June 17, 1997
APPLICATION NUMBER: U.S. 60/019,629

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; FILING DATE: June 17, 1996
; APPLICATION NUMBER: U.S. 60/023,485
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: U.S. 60/030,860
; FILING DATE: No. US20020169303A1ember 13, 1996
; APPLICATION NUMBER: U.S. 60/034,286
; FILING DATE: December 19, 1996
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: No. US20020169303A1ember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-087-993-36

Query Match 100.0%; Score 458; DB 13; Length 458;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRLSARSFLERLEARGREGAVLAGESFDIQACSAWKADGVCSTVAGSRPENVRKN 60
DB 1 MSRLSARSFLERLEARGREGAVLAGESFDIQACSAWKADGVCSTVAGSRPENVRKN 60

QY 61 RYKDVLPYDQTRVILSLQEGHSDYINGNFIISGVDGSLAYIATQGLPHTLLDFWRLVW 120
DB 61 RYKDVLPYDQTRVILSLQEGHSDYINGNFIISGVDGSLAYIATQGLPHTLLDFWRLVW 120

QY 121 EFGVKVILMACRIENGRKRCERYWAQEQEPLQTLGFCITLKEKWLNEIDMLRLTKVTF 180
DB 121 EFGVKVILMACRIENGRKRCERYWAQEQEPLQTLGFCITLKEKWLNEIDMLRLTKVTF 180

QY 181 QKESRSVYQLQYMSWDRGVPSPDHMLAMVEARLQSGPPLCHVCSAGGRTGVLC 240
DB 181 QKESRSVYQLQYMSWDRGVPSPDHMLAMVEARLQSGPPLCHVCSAGGRTGVLC 240

QY 241 TVDYVRQLLTQMIPTPDSFLDFVVLKMRKORPAAVQTESQYRFLYHTVAQMFCSLTQNAS 300
DB 241 TVDYVRQLLTQMIPTPDSFLDFVVLKMRKORPAAVQTESQYRFLYHTVAQMFCSLTQNAS 300

QY 301 PHYQNIKENCAPLYDDALFURTQALLAIPRPFGVLRISVPGSPCHAMADTYAEQKR 360
DB 301 PHYQNIKENCAPLYDDALFURTQALLAIPRPFGVLRISVPGSPCHAMADTYAEQKR 360

QY 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTTPRAQPGAAEDARGTLPGRVPADQSPAG 420
DB 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTTPRAQPGAAEDARGTLPGRVPADQSPAG 420

QY 421 SGAYEDVAGGAQTGGGLGFNLRIGRPKGRDPPAEWTRV 458
DB 421 SGAYEDVAGGAQTGGGLGFNLRIGRPKGRDPPAEWTRV 458

RESULT 2
US-10-243-687-7
; Sequence 7, Application US/10243687
; Publication No. US20030073120A1
; GENERAL INFORMATION:
; APPLICANT: Aoki, Naohito
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
; AND RELATED PRODUCTS AND METHODS

```

```

; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/243,687
; FILING DATE: 16-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,626A
; FILING DATE: 29-Oct-1999
; APPLICATION NUMBER: 08/951,260
; FILING DATE: October 16, 1997
; APPLICATION NUMBER: 60/030,860
; FILING DATE: No. US20030073120A1ember 13, 1996
; APPLICATION NUMBER: PCT/1897/00946
; FILING DATE: June 17, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 227/004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-243-687-7

Query Match 6.3%; Score 29; DB 14; Length 453;
Best Local Similarity 100.0%; Pred. No. 4.6e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 GAQTGGGLGFNLRIGRPKGRDPPAEWTRV 458
DB 425 GAQTGGGLGFNLRIGRPKGRDPPAEWTRV 453

RESULT 3
US-10-087-993-32
; Sequence 32, Application US/10087993
; Publication No. US20020169303A1
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; Aoki, Naohito
; Kim, Yeong Woong
; Wang, Hong Yang
; Chen, Zhengjun
; Naylor, Oliver
; Kharitonov, Alexei Igorevich
; TITLE OF INVENTION: NOVEL PTP20, PDE-2, BDP1, CLK,
; AND S1RP POLYPEPTIDES AND RELATED
; PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

```

```
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/087,993
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,150
; FILING DATE: June 17, 1997
; APPLICATION NUMBER: U.S. 60/019,629
; FILING DATE: June 17, 1996
; APPLICATION NUMBER: U.S. 60/023,485
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: U.S. 60/030,860
; FILING DATE: No. US20020169303A1ember 13, 1996
; APPLICATION NUMBER: U.S. 60/034,286
; FILING DATE: December 19, 1996
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: No. US20020169303A1ember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-087-993-32
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; Query Match 5.2%; Score 24; DB 13; Length 448;
; Best Local Similarity 100.0%; Pred. No. 3.2e-14;
; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 100 AYIATQGPLPHTLLDFWRLVWVFG 123
Db 100 AYIATQGPLPHTLLDFWRLVWVFG 123
;
; RESULT 4
US-10-340-288-13
; Sequence 13, Application US/10340288
; Publication No. US20030170855A1
; GENERAL INFORMATION:
; APPLICANT: Albert Einstein College of Medicine of Yeshiva University
; APPLICANT: ZHANG, Zhong-Yin
; APPLICANT: XIE, LaiPing
; APPLICANT: ZHANG, Yan-Ling
; TITLE OF INVENTION: A NOVEL PROTEIN TYROSINE PHOSPHATASE SUBSTRATE-TRAPPING DOUBLE
; FILE OF INVENTION: MUTANT AND USES THEREOF
; FILE REFERENCE: 96700/792
; CURRENT APPLICATION NUMBER: US/10/340,288
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/347,413
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 37
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-340-288-13
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; Query Match 4.4%; Score 20; DB 14; Length 20;
; Best Local Similarity 100.0%; Pred. No. 1.4e-11;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 VVLKMKQKQRPAAVQTEQYR 20
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; RESULT 5
US-09-801-368-280
; Sequence 280, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 280
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-801-368-280
;
; Query Match 2.6%; Score 12; DB 9; Length 750;
; Best Local Similarity 100.0%; Pred. No. 0.021;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 227 VHCSAGCGRTGV 238
Db 664 VHCSAGCGRTGV 675
;
; RESULT 6
US-10-369-493-22392
; Sequence 22392, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
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; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 22392
 ; LENGTH: 750
 ; TYPE: PRT
 ; ORGANISM: Saccharomyces cerevisiae
 US-10-369-493-22392

Query Match 2.6%; Score 12; DB 15; Length 750;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCAGCGRTGV 238
 Db 664 VHCAGCGRTGV 675

RESULT 7

US-10-087-684-94
 ; Sequence 94, Application US/10087684
 ; Publication No. US20040029116A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Rieger, Daniel K.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Casman, Stacie, J.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Li, Li
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Mishra, Vishnu
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Vernet, Corine A.M.
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Gangolli, Esha A.
 ; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-214 CIP
 ; CURRENT APPLICATION NUMBER: US/10/087,684
 ; CURRENT FILING DATE: 2003-03-10
 ; PRIOR APPLICATION NUMBER: 60/253,834
 ; PRIOR FILING DATE: 2000-11-29
 ; PRIOR APPLICATION NUMBER: 60/250,926
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: 60/264,180
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 60/274,194
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: 60/313,656
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: 60/327,456
 ; NUMBER OF SEQ ID NOS: 220
 ; SOFTWARE: CuraSeqlist version 0.1
 ; SEQ ID NO 94
 ; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Domain
 US-10-087-684-94

Query Match 2.4%; Score 11; DB 12; Length 235;
 Best Local Similarity 100.0%; Pred. No. 0.07;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 KRYKDVLPYD 69
 Db 4 KRYKDVLPYD 14

RESULT 8

US-10-218-779-94
 ; Sequence 94, Application US/10218779
 ; Publication No. US20040029222A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: MacDougall, John
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Stone, David
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Grosse, William
 ; APPLICANT: Alsobrook II, John
 ; APPLICANT: Lepley, Denise
 ; APPLICANT: Rieger, Daniel
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Casman, Stacie
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Boldog, Ferenc
 ; APPLICANT: Li, Li
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Mishra, Vishnu
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Shenoy, Suresh
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Gangolli, Esha
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-214
 ; CURRENT APPLICATION NUMBER: US/10/218,779
 ; CURRENT FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: 60/253,834
 ; PRIOR FILING DATE: 2000-11-29
 ; PRIOR APPLICATION NUMBER: 60/250,926
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: 60/264,180
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 60/313,656
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: 60/327,456
 ; PRIOR FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 216
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 94
 ; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-218-779-94

Query Match 2.4%; Score 11; DB 12; Length 235;
 Best Local Similarity 100.0%; Pred. No. 0.07;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 KRYKDVLPYD 69
 Db 4 KRYKDVLPYD 14

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RESULT 9
US-10-072-012-819
; Sequence 819, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zethusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taugier Jr, Raymond J.
; APPLICANT: Gusev, Vladimr Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 819
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Protein-tyrosine phosphatase Consensus Sequence
US-10-072-012-819

Query Match          2.4%; Score 11; DB 12; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      59 KNRKDVLPYD 69
Db      4 KNRKDVLPYD 14

RESULT 10
US-09-848-294-7
; Sequence 7, Application US/09848294
; Patent No. US20020049179A1
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. US20020049179A1el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; TITLE OF INVENTION: Adhesions and Uses Therefor
; FILE REFERENCE: CSHL90-04PZA
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 07/494,036
; PRIOR FILING DATE: 1990-03-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-7

Query Match          2.4%; Score 11; DB 9; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      59 KNRKDVLPYD 69
Db      4 KNRKDVLPYD 14

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US-10-293-231-7
; Sequence 7, Application US/10293231
; Publication No. US20030113294A1
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: ISOLATION OF A cDNA ENCODING A NOVEL
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE WHICH LOCALIZES
; TITLE OF INVENTION: TO FOCAL ADHESIONS AND USES THEREOF
; FILE REFERENCE: 200125.409C3
; CURRENT APPLICATION NUMBER: US/10/293,231
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 7
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-231-7

Query Match          2.4%; Score 11; DB 14; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      59 KNRKDVLPYD 69
Db      4 KNRKDVLPYD 14

RESULT 12
US-10-087-684-93
; Sequence 93, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
US-10-087-684-93

Query Match          2.4%; Score 11; DB 12; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      59 KNRKDVLPYD 69
Db      4 KNRKDVLPYD 14
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```

/ APPLICANT: MacDougall, John R.
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Ellerman, Karen
/ APPLICANT: Stone, David J.
/ APPLICANT: Grosse, William M.
/ APPLICANT: Rieger, Denise M.
/ APPLICANT: Rieger, Daniel K.
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Spytek, Kimberly A.
/ APPLICANT: Boldog, Ferenc L.
/ APPLICANT: Li, Li
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Mishra, Vishnu
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Tchernev, Velizar T.
/ APPLICANT: Zernhet, Corine A.M.
/ APPLICANT: Zernhusen, Bryan D.
/ APPLICANT: Malyankar, Uriel M.
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Gangolli, Esha A.
/ TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-214 CIP
/ CURRENT APPLICATION NUMBER: US/10/087,684
/ CURRENT FILING DATE: 2003-03-10
/ PRIOR APPLICATION NUMBER: 60/253,834
/ PRIOR FILING DATE: 2000-11-29
/ PRIOR APPLICATION NUMBER: 60/250,926
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: 60/264,180
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/274,194
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: 60/313,656
/ PRIOR FILING DATE: 2001-08-20
/ PRIOR APPLICATION NUMBER: 60/327,456
/ PRIOR FILING DATE: 2001-10-05
/ NUMBER OF SEQ ID NOS: 220
/ SOFTWARE: CuraSeqList version 0.1
/ SEQ ID NO 93
/ LENGTH: 263
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Domain
/ US-10-087-684-93

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/ APPLICANT: Burgess, Catherine
/ APPLICANT: Casman, Stacie
/ APPLICANT: Spytek, Kimberly
/ APPLICANT: Boldog, Ferenc
/ APPLICANT: Li, Li
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Mishra, Vishnu
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Shenoy, Suresh
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Tchernev, Velizar
/ APPLICANT: Vernet, Corine
/ APPLICANT: Zerhusen, Bryan
/ APPLICANT: Malyankar, Uriel
/ APPLICANT: Guo, Xiaojia
/ APPLICANT: Miller, Charles
/ APPLICANT: Gangolli, Esha
/ TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
/ FILE REFERENCE: 21402-214
/ CURRENT APPLICATION NUMBER: US/10/218,779
/ CURRENT FILING DATE: 2002-08-14
/ PRIOR APPLICATION NUMBER: 60/253,834
/ PRIOR FILING DATE: 2000-11-29
/ PRIOR APPLICATION NUMBER: 60/250,926
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: 60/264,180
/ PRIOR FILING DATE: 2001-01-25
/ PRIOR APPLICATION NUMBER: 60/313,656
/ PRIOR FILING DATE: 2001-08-20
/ PRIOR APPLICATION NUMBER: 60/327,456
/ PRIOR FILING DATE: 2001-10-05
/ NUMBER OF SEQ ID NOS: 216
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 93
/ LENGTH: 263
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-218-779-93

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QY 59 KURYKDVLPYD 69
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 DB 30 KURYKDVLPYD 40

RESULT 13
 US-10-218-779-93
 ; Sequence 93, Application US/10218779
 ; Publication No. US20040029222A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: MacDougall, John
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Stone, David
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Grosse, William
 ; APPLICANT: Alsobrook II, John
 ; APPLICANT: Lepley, Denise
 ; APPLICANT: Rieger, Daniel

Db 15 KNRYKDVLPYD 25

RESULT 15

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RES001 13
US-10-309-423-4
; Sequence 4, Application US/10309423
; Publication No. US20040006777A1
; GENERAL INFORMATION:
; APPLICANT: HSC Research and Development Limited Partnership
; TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases
; FILE OF INVENTION: 92906-2
; CURRENT APPLICATION NUMBER: US/10/309,423
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/600,358
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: CA 2,220,853
; PRIOR FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-423-4

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Query Match          2.4%; Score 11; DB 15; Length 692;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 228 HCSAGCGRTGV 238
|||
Db 226 HCSAGCGRTGV 236

Search completed: August 17, 2004, 20:58:15
Job time : 47 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:49:12 ; Search time 16 Seconds
(without alignments)
2753.482 Million cell updates/sec

Title: US-10-087-993A-36
Perfect score: 458
Sequence: 1 MRSRLSARSFLERLEARGG.....NLRIKPKGRDPPEWTRV 458

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	2.6	750	2 S67100	protein-tyrosine-p
2	11	2.4	303	1 S28392	protein-tyrosine-p
3	11	2.4	802	1 B44390	protein-tyrosine-p
4	11	2.4	913	1 A41109	protein-tyrosine-p
5	11	2.4	928	2 S50578	hypothetical prote
6	11	2.4	1132	2 T49403	related to protein
7	11	2.4	1187	1 JC4155	protein-tyrosine-p
8	11	2.4	1189	1 JC2366	protein-tyrosine-p
9	10	2.2	248	2 T46903	hypothetical prote
10	10	2.2	340	2 T51846	protein-tyrosine-p
11	10	2.2	340	2 C96741	hypothetical prote
12	10	2.2	382	1 S48748	protein-tyrosine-p
13	10	2.2	582	2 A57068	protein-tyrosine-p
14	10	2.2	597	2 B53978	protein-tyrosine-p
15	10	2.2	694	2 A53978	protein-tyrosine-p
16	10	2.2	773	1 JH0609	protein-tyrosine-p
17	10	2.2	775	2 S55345	protein-tyrosine-p
18	10	2.2	780	1 JC1368	protein-tyrosine-p
19	10	2.2	1015	2 JC5283	transmembrane tyro
20	10	2.2	1015	2 JC5082	phogrin precursor
21	10	2.2	1262	1 B48758	protein-tyrosine-p
22	10	2.2	1290	2 A56493	leucocyte common a
23	10	2.2	1437	2 T31093	probable protein-t
24	10	2.2	1496	1 A48758	protein-tyrosine-p
25	10	2.2	1499	2 I50212	protein-tyrosine-p
26	10	2.2	1501	2 I58148	protein-tyrosine-p
27	10	2.2	1863	2 S46217	protein-tyrosine-p
28	10	2.2	1897	1 TDHULK	leukocyte antigen-
29	10	2.2	1898	2 S46216	leukocyte antigen-

RESULT 1

S67100

protein-tyrosine-phosphatase (EC 3.1.3.48) PTP2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O4849; protein YOR208W
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 21-Jul-2000
C;Accession: S67100; A42667; A41980; S31554; S14170; JCL484; S42155

R;Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996

A;Reference number: S66685
A;Accession: S67100
A;Molecule type: DNA

A;Residues: 1-750 <HUG>
A;Cross-references: EMBL:275116; NID:G1420486; PID:e252394; PID:G1420487; MIPS:YOR208W

A;Experimental source: strain S288C
R;Guan, K.L.; Deschenes, R.J.; Dixon, J.E.
J. Biol. Chem. 267, 10024-10030, 1992

A;Title: Isolation and characterization of a second protein tyrosine phosphatase gene, P1
A;Reference number: A42667; MUID:92250559; PMID:1577774
A;Accession: A42667

A;Molecule type: DNA
A;Residues: 1-473, NV, 476-750 <GUA>
A;Cross-references: GB:M85287

R;Ota, I.M.; Varshavsky, A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2355-2359, 1992

A;Title: A gene encoding a putative tyrosine phosphatase suppresses lethality of an N-enc
A;Reference number: A41980; MUID:92196117; PMID:1549598
A;Accession: A41980

A;Molecule type: DNA
A;Residues: 1-750 <OTA>

A;Cross-references: EMBL:M82872; NID:G172293; PIDN:AAA4922.1; PID:G172294
A;Note: sequence extracted from NCBI backbone (NCBIN:88405, NCBI:88407)
R;James, P.; Hall, B.D.; Whelen, S.; Craig, E.A.

submitted to the EMBL Data Library, July 1991

A;Description: Multiple protein tyrosine phosphatase-encoding genes in the yeast Sacchar
A;Reference number: S31554
A;Accession: S31554

A;Molecule type: DNA
A;Residues: 1-370, 'S', 372-659, 'GA', 662-750 <JAM>

A;Cross-references: EMBL:M38723; NID:G172381; PID:G172382
R;James, P.; Whelen, S.; Hall, B.D.
J. Biol. Chem. 266, 5616-5624, 1991

A;Title: The RFI1 gene of yeast encodes the second-largest subunit of RNA polymerase III
A;Reference number: S14169; MUID:91170230; PMID:2005101
A;Accession: S14170

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-67 <JBI>

A;Cross-references: EMBL:M38723
R;James, P.; Hall, B.D.; Whelen, S.; Craig, E.A.
Gene 122, 101-110, 1992

A;Title: Multiple protein tyrosine phosphatase-encoding genes in the yeast Saccharomyces

A:Reference number: JC1484; MUID:93083970; PMID:1452018
 A:Accession: JC1484
 A:Molecule type: DNA
 A:Residues: 1-370,'S',372-659,'GA',662-750 <JAW>
 C:Genetics:

A:Gene: SGD,PTP2
 A:Cross-references: SGD:S0005734; MIPS:YOR208w
 A:Map position: 15R

C:Superfamily: protein-tyrosine-phosphatase homology
 C:Keywords: cell division control; nucleotide binding; phosphoprotein; phosphoric monoester
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 F:669-674/Region: nucleotide binding #status predicted
 F:666/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:662/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.6%; Score 12; DB 2; Length 750;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCAGCGRTGV 238

|||||

Db 664 VHCAGCGRTGV 675

RESULT 2

S28392
 C:Protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type pyp3 - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Dec-1999
 C:Accession: S28392; T37537
 F:Miller, J.B.A.; Lemaers, G.; Russell, P.
 EMBO J. 11, 4933-4941, 1992

A:Title: Pyp3 PTPase acts as a mitotic inducer in fission yeast.

A:Reference number: S28392; MUID:93099868; PMID:1464318

A:Accession: S28392

A:Molecule type: DNA

A:Residues: 1-303 <ML>

A:Cross-references: EMBL:X69994; NID:G5017; PIDN:CAA49609.1; PID:G5018

R:Murphy, L.; Harris, D.; Barrall, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, August 1997

A:Reference number: Z21721

A:Accession: T37537

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-303 <MR>

A:Cross-references: EMBL:Z98595; PIDN:CAB11188.1; GSPDB:GN00066; SPDB:SPAC11E3.09

A:Experimental source: strain 972h-; coemid c11E3

C:Genetics:

A:Gene: pyp3

A:Map position: 1

A:Introns: 96/3

C:Superfamily: Schizosaccharomyces protein-tyrosine-phosphatase, nonreceptor type pyp3;
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:49-281/Domain: protein-tyrosine-phosphatase homology <PTP>

F:227/Active site: Cys (phosphocysteine intermediate) #status predicted

F:233/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.4%; Score 11; DB 1; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCAGCGRTG 237

|||||

Db 225 VHCAGCGRTG 235

RESULT 3

B44390

Protein-tyrosine-phosphatase (EC 3.1.3.48) PEP, nonreceptor type 8 - mouse

N:Alternate names: protein-tyrosine-phosphatase PEP

C:Species: Mus musculus (house mouse)

C:Date: 03-May-1994 #sequence_revision 26-May-1994 #text_change 11-Jun-1999

C:Accession: B44390; S71952; S27876

R:Matthews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L.

Mol. Cell. Biol. 12, 2396-2405, 1992

A:Title: Characterization of hematopoietic intracellular protein tyrosine phosphatases: Csk, and threonine-rich sequences.

A:Reference number: A44390; MUID:92236615; PMID:1373816

A:Accession: B44390

A:Molecule type: mRNA

A:Residues: 1-802 <Maf>

A:Cross-references: GB:M90388; NID:G200522; PIDN:AAA39994.1; PID:G200523

R:Cloutier, J.F.; Veillette, A.

EMBO J. 15, 4909-4918, 1996

A:Title: Association of inhibitory tyrosine protein kinase p50(csk) with protein tyrosine phosphatase

A:Reference number: S71952; MUID:97045099; PMID:8890164

A:Accession: S71952

A>Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 495-789 <CLO>

C:Comment: This protein is found primarily in hematopoietic tissues.

C:Genetics:

A:Gene: 702pep

C:Complex: Physically associates with inhibitory tyrosine protein kinase Csk; interaction

C:Function:

A:Description: probably an effector and/or regulator of tyrosine protein kinase csk in T-

C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 8; protein-tyrosine-phosphatase

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:54-278/Domain: protein-tyrosine-phosphatase homology <PTP>

F:497-802/Region: glutamic acid/proline/serine/threonine-rich

F:613-621/Region: proline-rich

F:688-695/Region: proline-rich

F:227/Active site: Cys (phosphocysteine intermediate) #status predicted

F:233/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.4%; Score 11; DB 1; Length 802;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 228 HCSAGCGRTGV 238

|||||

Db 226 HCSAGCGRTGV 236

RESULT 4

A41109

Protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN3, nonreceptor type 3 [validated] - human

N:Alternate names: PTPH1

C:Species: Homo sapiens (man)

C:Date: 27-Mar-1992 #sequence_revision 02-May-1994 #text_change 21-Jun-2002

A:Accession: A41109; I55698

R:Yang, Q.; Tonks, N.K.

Proc. Natl. Acad. Sci. U.S.A. 88, 5949-5953, 1991

A:Title: Isolation of a cDNA clone encoding a human protein-tyrosine phosphatase with hom

A:Reference number: A41109; MUID:91296738; PMID:1648725

A:Accession: A41109

A:Molecule type: mRNA

A:Residues: 1-913 <YAN>

A:Cross-references: GB:M64572; NID:G179912; PIDN:AAA35647.1; PID:G179913

J. Gastroenterol. 29, 727-732, 1994

A:Title: Expression of cytoskeletal-associated protein tyrosine phosphatase PTPH1 mRNA in

A:Reference number: I55698; MUID:95179278; PMID:7874267

A:Accession: I55698

A>Status: translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 899-913 <RES>

A:Cross-references: GB:S76309; NID:G913165; PIDN:AAB33583.1; PID:G913166

C:Genetics:

A:Gene: GDB:PTPN3

A:Cross-references: GDB:I13386; OMIM:176877

A:Map position: 9c31-9c31

C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; p

C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase

F:31-308/Domain: protein 4.1 membrane-binding domain homology <B41>

F:516-590/Domain: GLGF domain homology <GLG>

F;670-990/Domain: protein-tyrosine-phosphatase homology <PTP>
F;842/Active site: Cys (phosphocysteine intermediate) #status predicted
F;848/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.4%; Score 11; DB 1; Length 913;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 KNRYKDVLPYD 69
Db 673 KNRYKDVLPYD 683
|||||

RESULT 5
S50578
hypothetical protein YER075c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001
C;Accession: S50578
R;Dietrich, F.S.
Submitted to: The EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae lambda clone 3612 and cosmid 9747.
A;Reference number: S50438
A;Accession: S50578
A;Molecule type: DNA
A;Residues: 1-928 <DIE>
A;Cross-references: EMBL:U18814; NID:g603309; PIDN:AA564614.1; PID:g603312; MIPS:YER075c
C;Genetics:
A;Gene: SGD:PTP3
A;Cross-references: SGD:S0000877; MIPS:YER075c
A;Map position: 5R
C;Superfamily: protein-tyrosine-phosphatase homology
C;Keywords: phosphoprotein
F;527-867/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;804/Active site: Cys (phosphocysteine intermediate) #status predicted
F;810/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.4%; Score 11; DB 2; Length 928;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCSAGCGRTG 237
Db 802 VHCSAGCGRTG 812
|||||

RESULT 6
T49403
related to protein-tyrosine-phosphatase [imported] - Neurospora crassa
N;Alternate names: protein BID4.180
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49403
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
A;Accession: T49403
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1132 <SCH>
A;Cross-references: EMBL:AL355928; GSPDB:GN00116; NCSP:B1D4.180
A;Experimental source: BAC clone BID4; strain OR74A
C;Genetics:
A;Gene: NCSP:B1D4.180
A;Map position: 6
A;Introns: 670/3; 1104/2

Query Match 2.4%; Score 11; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCSAGCGRTG 237
Db 802 VHCSAGCGRTG 812
|||||

Db 904 VHCSAGCGRTG 914

RESULT 7
JC4155
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - human
N;Alternate names: PEZ protein; protein-tyrosine-phosphatase/ezzrin-like protein
C;Species: Homo sapiens (man)
C;Date: 27-Aug-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
C;Accession: JC4155
R;Smith, A.L.; Mitchell, P.J.; Shipley, J.; Gusterson, B.A.; Rogers, M.V.; Crompton, M.R. Biochem. Biophys. Res. Commun. 209, 959-965, 1995
A;Title: PEZ: a novel human cDNA encoding protein tyrosine phosphatase-and ezrin-like domain
A;Reference number: JC4155; MUID:95251727; PMID:7733990
A;Accession: JC4155
A;Molecule type: mRNA
A;Residues: 1-1187 <SMI>
A;Cross-references: EMBL:X82676; NID:g3929753; PIDN:CAA57993.1; PID:g805029
A;Experimental source: breast
C;Genetics:
A;Gene: GDB:PTPN14
A;Cross-references: GDB:454485
A;Map position: lq32-2-lq32-2
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;23-302/Domain: protein 4.1 membrane-binding domain homology <B41>
F;566-575/Region: proline-rich
F;709-716/Region: acidic
F;933-1169/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1121/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1121/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.4%; Score 11; DB 1; Length 1187;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 YIATQGLPHT 111
Db 979 YIATQGLPHT 989
|||||

RESULT 8
JC2366
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - mouse
N;Alternate names: PEZ protein; protein-tyrosine-phosphatase PTP36; protein-tyrosine-phos
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
C;Accession: JC2366
R;Sawada, M.; Ogata, M.; Fujino, Y.; Hamaoka, T.
Biochem. Biophys. Res. Commun. 203, 479-484, 1994
A;Title: cDNA cloning of a novel protein tyrosine phosphatase with homology to cytoskeleton
A;Reference number: JC2366; MUID:94354845; PMID:8074693
A;Accession: JC2366
A;Molecule type: mRNA
A;Residues: 1-1189 <SAW>
A;Cross-references: GB:D31842; NID:g507330; PIDN:BAAC6628.1; PID:g507331
A;Experimental source: thymus
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;23-302/Domain: protein 4.1 membrane-binding domain homology <B41>
F;566-575/Region: proline-rich
F;712-718/Region: acidic
F;935-1171/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1123/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1123/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.4%; Score 11; DB 1; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 YIATQGLPHT 111
Db 981 YIATQGLPHT 991
|||||

```

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C96741
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-248 <AAA>
A:Cross-references: EMBL:AL157451
A:Reference number: 224134
A:Genetics:
A:Note: DKFZp761A0712.1
C:Superfamily: protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphatase
Query Match 2.2%; Score 10; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AYIATQGPLP 109
DB 48 AYIATQGPLP 57

RESULT 10
T51846
protein-tyrosine-phosphatase (EC 3.1.3.48) 1 [validated] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
C:Accession: T51846
R:Xu, Q.; Fu, H.H.; Gupta, R.; Luan, S.
Plant Cell 10, 849-857, 1998
A:Title: Molecular characterization of a tyrosine-specific protein phosphatase encoded b
A:Reference number: 225483; MUID:98259006; PMID:9596642
A:Accession: T51846
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-340 <XUQ>
A:Cross-references: EMBL:AF055635; PIDN:AAC68859.1
A:Note: PTP1
C:Function:
A:Description: (EC 3.1.3.48) [validated, MUID:98259006]; specifically hydrolyzes phospho
C:Superfamily: Dictyostelium protein-tyrosine-phosphatase, nonreceptor type 2; protein-t
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas

Query Match 2.2%; Score 10; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 IATQGPLEPT 111
DB 135 IATQGPLEPT 144

RESULT 11
C96741
Hypothetical protein F14023.24 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C:Accession: C96741
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

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Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C96741
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-340 <STO>
A:Cross-references: GB:AE005173; NID:97239513; PIDN:AAF43239.1; GSPDB:GN00141
C:Genetics:
A:Gene: F14023.24
A:Map position: 1
A:Superfamily: Dictyostelium protein-tyrosine-phosphatase, nonreceptor type 2; protein-t)
Query Match 2.2%; Score 10; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 IATQGPLEPT 111
DB 135 IATQGPLEPT 144

RESULT 12
S48748
protein-tyrosine-phosphatase (EC 3.1.3.48), probable nonreceptor type 12 splice form - r
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: S48748
R:Moriyama, T.; Kawanishi, S.; Inoue, T.; Imai, E.; Kaneko, T.; Xia, C.; Takenaka, M.; No
FEBS Lett. 353, 305-308, 1994
A:Title: cDNA cloning of a cytosolic protein tyrosine phosphatase (RKPTP) from rat kidney
A:Reference number: S48748; MUID:95046282; PMID:7957881
A:Accession: S48748
A:Molecule type: mRNA
A:Residues: 1-382 <MOR>
A:Cross-references: GB:D38072; NID:9567262; PIDN:BAA07266.1; PID:G699627
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosph
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:58-282/Domain: protein-tyrosine-phosphatase homology <PTP>
F:231/Active site: Cys (phosphocysteine intermediate) #status predicted
F:237/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.2%; Score 10; DB 1; Length 382;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 HCSAGCGRTG 237
DB 230 HCSAGCGRTG 239

RESULT 13
A57068
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)
N:Alternate names: leukocyte antigen-related protein LAR
C:Species: Mus musculus (house mouse)
C>Date: 03-Oct-1995 #sequence_revision 09-Mar-1996 #text_change 23-Jul-1999
C:Accession: A57068; S40280
R:Schaapveld, R.O.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis, D.;
Genomics 27, 124-130, 1995
A:Title: The mouse gene Ptpfr encoding the leukocyte common antigen-related molecule LAR.
A:Reference number: A57068; MUID:9539448; PMID:7685159
A:Accession: A57068
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-582 <SCH>
A:Cross-references: GB:D37988; NID:993005; PIDN:CAA86070.1; PID:G993006
R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
Submitted to the EMBL Data Library, June 1993
A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
A:Reference number: S40280

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A;Accession: S40280
A;Molecule type: mRNA
A;Residues: 116-221 <HEN>
A;Cross-references: EMBL:Z23049; NID:g438135; PIDN:CAA80584.1; PID:g438136
C;Genetics:
A;Gene: Ptpfr
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
OgY
C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
F;1-582/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC>
F;50-271/Domain: protein-tyrosine-phosphatase homology <PTP>
F;339-562/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;223/Active site: Cys (phosphocysteine intermediate) #status predicted
F;229/Binding site: substrate phosphate (Arg) #status predicted
F;514/Active site: Cys (phosphocysteine intermediate) #status predicted
F;520/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.2%; Score 10; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 0.2; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0

Qy 100 AYIATQGFLP 109
Db 94 AYIATQGFLP 103
|||||

RESULT 14
B53978
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type PTPX10 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
C;Accession: B53978
R;Del Vecchio, R.L.; Tonks, N.K.
J. Biol. Chem. 269, 19639-19645, 1994
A;Title: Characterization of two structurally related Xenopus laevis protein tyrosine ph
A;Reference number: A53978; MUID:94308257; PMID:8034733
A;Accession: B53978
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-597
A;Cross-references: GB:L33099; NID:g495671; PIDN:AAA1728.1; PID:g495672
A;Experimental source: ovary
A;Note: sequence extracted from NCBI backbone (NCBI:149759, NCBI:149760)
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinaldehyde-
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;38-227/Domain: cellular retinaldehyde-binding protein homology <CRB>
F;328-564/Domain: protein-tyrosine-phosphatase homology <PTP>
F;516/Active site: Cys (phosphocysteine intermediate) #status predicted
F;522/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.2%; Score 10; DB 2; Length 597;
Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0

Qy 100 AYIATQGFLP 109
Db 372 AYIATQGFLP 381
|||||

RESULT 15
A53978
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type PTPX1 - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 24-Apr-1998
C;Accession: A53978
R;Del Vecchio, R.L.; Tonks, N.K.
J. Biol. Chem. 269, 19639-19645, 1994
A;Title: Characterization of two structurally related Xenopus laevis protein tyrosine ph
A;Reference number: A53978; MUID:94308257; PMID:8034733
A;Accession: A53978
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-694

A;Experimental source: ovary
A;Note: sequence extracted from NCBI backbone (NCBI:149756, NCBI:149758)
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinaldehyde-
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
F;38-227/Domain: cellular retinaldehyde-binding protein homology <CRB>
F;425-561/Domain: protein-tyrosine-phosphatase homology <PTP>
F;613/Active site: Cys (phosphocysteine intermediate) #status predicted
F;619/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.2%; Score 10; DB 2; Length 694;
Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0

Qy 100 AYIATQGFLP 109
Db 469 AYIATQGFLP 478
|||||

Search completed: August 17, 2004, 20:53:05
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:44:41 ; Search time 14 Seconds
(without alignments)

1703.438 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 458

Sequence: 1 MSRLSDARSFLERLARGG.....NLRIKRPKGRDPPAEWTRV 458

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	458	100.0	458	PTNI_HUMAN	Q9952 homo sapien
2	12	2.6	750	PTP2_YEAST	P29461 saccharomyc
3	11	2.4	303	PTP3_SCHPO	P32587 schizosacch
4	11	2.4	802	PTN8_MOUSE	P29352 mus musculu
5	11	2.4	807	PTNM_HUMAN	Q9Y2r2 homo sapien
6	11	2.4	913	PTN3_HUMAN	P26045 homo sapien
7	11	2.4	928	PTP3_YEAST	P40048 saccharomyc
8	11	2.4	1187	PTNE_HUMAN	Q15678 homo sapien
9	11	2.4	1189	PTNE_MOUSE	Q62130 mus musculu
10	10	2.2	775	PTNC_MOUSE	P35831 mus musculu
11	10	2.2	780	PTNC_HUMAN	Q05209 homo sapien
12	10	2.2	1001	PTPX_MOUSE	P80560 mus musculu
13	10	2.2	1004	PTPX_RAT	O63475 rattus norv
14	10	2.2	1013	PTPX_MAGNE	O02895 macaca neme
15	10	2.2	1015	PTPF_HUMAN	Q92932 homo sapien
16	10	2.2	1897	PTPF_HUMAN	P10586 homo sapien
17	10	2.2	1948	PTNS_HUMAN	Q13332 homo sapien
18	9	2.0	979	PTPN_BOVIN	P56722 bos taurus
19	9	2.0	979	PTPN_HUMAN	Q16849 homo sapien
20	9	2.0	979	PTPN_MOUSE	Q60673 mus musculu
21	9	2.0	983	PTPN_RAT	Q63259 rattus norv
22	9	2.0	1216	PTPO_HUMAN	Q16827 homo sapien
23	9	2.0	1422	PTPG_CHICK	Q98936 gallus gall
24	9	2.0	1442	PTPG_MOUSE	Q05909 mus musculu
25	9	2.0	1445	PTPG_HUMAN	P23470 homo sapien
26	9	2.0	1912	PTPD_HUMAN	P23468 homo sapien
27	9	2.0	2200	LAR_CAEL	Q9bmh8 caenorhabd
28	8	1.7	294	HDL_BRANA	P46606 brassica na
29	8	1.7	601	SG2_RANRI	P30945 rana ridibu
30	8	1.7	764	GLGB_ANASP	Q8YX99 anabaena sp
31	8	1.7	1174	PTNL_HUMAN	Q16825 homo sapien
32	8	1.7	1175	PTNL_RAT	Q62728 rattus norv
33	8	1.7	1176	PTNL_MOUSE	Q62136 mus musculu

ALIGNMENTS

RESULT 1

ID	PTNI_HUMAN	STANDARD	PRT	458 AA.
AC	Q9952;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Protein-tyrosine phosphatase, non-receptor type 18 (EC 3.1.3.48)			
DE	(Brain-derived phosphatase).			
GN	PTPN18 OR BDPI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND CHARACTERIZATION.			
RP	TISSUE=Brain;			
RC	MEDLINE=97108674; PubMed=8950995;			
RX	Kim Y.W., Wang H.Y., Sures I., Lammers R., Martell K.J., Ullrich A.;			
RA	"Characterization of the PEST family protein tyrosine phosphatase			
RT	BDPI."			
RL	Oncogene 13:2275-2279(1996).			
CC	FUNCTION: Differentially dephosphorylate autophosphorylated			
CC	tyrosine kinases which are known to be overexpressed in tumor			
CC	tissues.			
CC	CAATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein			
CC	tyrosine + phosphate.			
CC	TISSUE SPECIFICITY: Expressed in brain, colon and several tumor-			
CC	derived cell lines.			
CC	SIMILARITY: Belongs to the protein-tyrosine phosphatase family.			
CC	Non-receptor class subfamily.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; X79568; CAA56105.1; ..			
DR	HSSP; Q06124; 2SHP.			
DR	Genew; HGNC:9649; PTPN18.			
DR	MIM; 606587; ..			
DR	GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. .; TAS.			
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.			
DR	InterPro; IPR000387; TYR phosphatase.			
DR	InterPro; IPR000242; TYR PP.			
DR	Pfam; PF00102; Y phosphatase; 1.			
DR	PRINTS; PR00700; PRTYPHPTASE.			
DR	SMART; SM00194; PTPC; 1.			
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.			
DR	PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.			
DR	PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 1.			
KW	Hydrolase.			
DOMAIN	26 291			PROTEIN-TYROSINE PHOSPHATASE.

34	8	1.7	1238	1	PTPJ_MOUSE	Q64455 mus musculu
35	8	1.7	1337	1	PTPJ_HUMAN	Q12913 homo sapien
36	8	1.7	1705	1	PTPV_MOUSE	P70289 mus musculu
37	8	1.7	1711	1	PTPV_RAT	O64612 rattus norv
38	7	1.5	109	1	UCN2_RAT	O91ww1 rattus norv
39	7	1.5	109	1	Y85A_METJA	P81315 methanococc
40	7	1.5	112	1	UCN2_MOUSE	Q99m18 mus musculu
41	7	1.5	158	1	DHSD_BOVIN	Q95123 bos taurus
42	7	1.5	191	1	R19_AGRIS	Q8ugf0 agrobacteri
43	7	1.5	191	1	R19_RHIME	Q92q29 rhizobium m
44	7	1.5	192	1	RL9_RHILT	Q9f9k6 rhizobium l
45	7	1.5	201	1	SDC2_RAT	P34900 rattus norv

	FT	ACT_SITE	229	229	PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).	
	FT	SEQUENCE	458 AA;	50384 MW;	46BCA1E17C2C78B1 CRC64;	
	SQ	Query Match	100.08;	Score 458;	DB 1; Length 458;	
		Best Local Similarity	100.08;	Pred. No. 0;	Mismatches 0; Indels 0; Gaps 0;	
		Matches 458;	Conservative 0;			
QY		1	MSRSLDSARSFLERLEARGREGVAVLAGEFSDIQACSAAMKADGCSTVAGSRPENVRKN	60		
Db		1	MSRSLDSARSFLERLEARGREGVAVLAGEFSDIQACSAAMKADGCSTVAGSRPENVRKN	60		
QY		61	RKYDVLPTDQTRVILSLLQEGHSDYNGNIRGVGDSLAYIATQGPLPHTILDFFRLVM	120		
Db		61	RKYDVLPTDQTRVILSLLQEGHSDYNGNIRGVGDSLAYIATQGPLPHTILDFFRLVM	120		
QY		121	EPGVKVILMACREIENGKRERYMAOBEPLQTGLFCITILIKEKWLINEDIMLRTLKVT	180		
Db		121	EPGVKVILMACREIENGKRERYMAOBEPLQTGLFCITILIKEKWLINEDIMLRTLKVT	180		
QY		181	QKESRSVTOQLQMSWPDGRVSSPDHMLAMVEEARLRQGGPEPLCVHCAGCGRTGVLC	240		
Db		181	QKESRSVTOQLQMSWPDGRVSSPDHMLAMVEEARLRQGGPEPLCVHCAGCGRTGVLC	240		
QY		241	TVDVYRQLLLTQMIPPDFSLFDVVLKMRKPAPAAVQTEEQRYFLYHYTVQAQMF CSTLNAS	300		
Db		241	TVDVYRQLLLTQMIPPDFSLFDVVLKMRKPAPAAVQTEEQRYFLYHYTVQAQMF CSTLNAS	300		
QY		301	PHYQNIKENCAPLYDDALFLTTPQALLAI PRPPGGVLRISIVPGSPGHAMADTYABEQXR	360		
Db		301	PHYQNIKENCAPLYDDALFLTTPQALLAI PRPPGGVLRISIVPGSPGHAMADTYABEQXR	360		
QY		361	GAPAGAGSGTGCTGTGARSAAEAPLSKYVTPRAQRPCAAEADEARGLTCRVPADQSPAG	420		
Db		361	GAPAGAGSGTGCTGTGARSAAEAPLSKYVTPRAQRPCAAEADEARGLTCRVPADQSPAG	420		
QY		421	SGAYEDVAGGAQTGGLGFNLRIAGRPKGRDP PPAEWTRV	458		
Db		421	SGAYEDVAGGAQTGGLGFNLRIAGRPKGRDP PPAEWTRV	458		
RESULT 2						
PTP2_YEAST						
ID	PTP2_YEAST	STANDARD;	PRT;	750 AA.		
AC	P29461;					
DT	01-APR-1993	(Rel. 25, Created)				
DT	01-APR-1993	(Rel. 25, Last sequence update)				
DT	10-OCT-2003	(Rel. 42, Last annotation update)				
DE	Protein-tyrosine phosphatase 2 (EC 3.1.3.48) (PTPase 2).					
GN	PTP2 OR YOR208W.					
OS	Saccharomyces cerevisiae (Baker's yeast).					
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;					
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.					
OX	NCBI_TaxID=4932;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=92250559; PubMed=1577774;					
RT	Guan K., Deschenes R.J., Dixon J.E.;					
RT	"Isolation and characterization of a second protein tyrosine					
RT	phosphatase gene, PTP2, from Saccharomyces cerevisiae.";					
RL	J. Biol. Chem. 267:10024-10030(1992).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=92196117; PubMed=1549598;					
RT	Ota I.M., Varshavsky A.;					
RT	"A gene encoding a putative tyrosine phosphatase suppresses lethality					
RT	of an N-end rule-dependent mutant.";					
RL	Proc. Natl. Acad. Sci. U.S.A. 89:2355-2359(1992).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RX	James P., Hall B.D., Whelen S., Craig E.A.;					
RA	Submitted (JUL-1991) to the EMBL/GenBank/DBSJ databases.					
RT	"Py3 PTPase acts as a mitotic inducer in fission yeast.";					
RN	[4]					
RP	SEQUENCE FROM N.A.					
RA	Hughes B., Pohl T.M.;					
RL	Submitted (JUL-1996) to the EMBL/GenBank/DBSJ databases.					
CC	-!- FUNCTION: May be implicated in the ubiquitin-mediated protein degradation pathway. May be involved in the regulation of MAP kinase FUS3					
CC	-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.					
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.					
CC	-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Non-receptor class subfamily.					
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EMBL:	M85287; -- NOT ANNOTATED_CDS.					
EMBL:	M82872; AAA34322.1; --					
EMBL:	M38723; AAB59323.1; --					
EMBL:	Z75116; CAA99423.1; --					
PIR:	S67100; S67100.					
HSSP:	P18052; 1YFO.					
GeneOnline:	143796; --					
SGD:	S0005734; PTP2.					
GO:	GO:0005634; C:nucleus; IDA.					
InterPro:	IP					

```

RL EMBO J. 11:4933-4941(1992).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Brooks J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Sgroves K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagals K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squires R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Taves A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer B., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gallibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Ravuelta J.B., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shipakovski G.V., Usery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
CC Nature 415:871-880(2002).
CC
CC -1- FUNCTION: Contributes to dephosphorylation of tyrosine 15 of
CC cdc2.
CC
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC
CC Non-receptor class subfamily.
CC
CC -----
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CC -----
CC EMBL; X69994; CAA49609.1; -.
CC EMBL; Z98595; CAB1188.1; -.
CC PIR; P28392; S28392.
CC HSP; P28827; 1RPM.
CC GeneDB Spombe; SPAC11E3.09; -.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00700; PRTPHPPTASE.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
CC KW Hydrolyase; 3D-structure.
CC FT DOMAIN; 23 288
CC FT ACT_SITE; 227 227
CC FT ACT_SITE; 227 227
CC FT ACT_SITE; 227 227
CC SQ SEQUENCE 303 AA; 34583 MW; 6BD642C818B32791 CRC64;

Query Match 2.4%; Score 11; DB 1; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCAGCGRTG 237
Db 225 VHCAGCGRTG 235

RESULT 5
ID PTNM HUMAN STANDARD; PRT; 807 AA.
AC Q9Y2R2; O95063; O95064;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

RESULT 4
ID PTN8 MOUSE STANDARD; PRT; 802 AA.
AC P29352;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 8 (EC 3.1.3.48)
DE (Hematopoietic cell protein-tyrosine phosphatase 70Z-PEP).
GN PTPN8
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92236615; PubMed=1373816;
RA Matthews R.J., Bowne D.B., Flores E., Thomas M.L.;
RT "Characterization of hematopoietic intracellular protein tyrosine
RT phosphatases: description of a phosphatase containing an SH2 domain
RT and another enriched in proline-, glutamic acid-, serine-, and
RT threonine-rich sequences."
RT Mol. Cell. Biol. 12:2396-2405(1992).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC
CC -1- TISSUE SPECIFICITY: Spleen, thymus, lymph node and bone marrow.
CC
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC
CC Non-receptor class subfamily.
CC
CC -----
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CC -----
CC EMBL; M90388; AAA39994.1; -.
CC PIR; B44390; B44390.
CC PDB; 1JEG; 31-OCT-01.
CC MGD; MGI:107170; Ptpn8.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00700; PRTPHPPTASE.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
CC KW Hydrolyase; 3D-structure.
CC FT DOMAIN; 23 288
CC FT ACT_SITE; 227 227
CC FT ACT_SITE; 227 227
CC FT ACT_SITE; 227 227
CC SQ SEQUENCE 802 AA; 89714 MW; 0F1E4539BD4613E CRC64;

Query Match 2.4%; Score 11; DB 1; Length 802;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 228 HCSAGCGRTGV 238
Db 226 HCSAGCGRTGV 236

RESULT 5
ID PTNM HUMAN STANDARD; PRT; 807 AA.
AC Q9Y2R2; O95063; O95064;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
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DR EMBL; S76309; AAB33583.1; -.
DR PIR; A41109; A41109.
DR HSP; P18031; LPTV.
DR Genew; HGNC:9655; PTPN3.
DR MM; 176877; -.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000293; Band 4.1.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00373; Band 41; 1.
DR Pfam; PF00595; PDZ_1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00335; BAND41.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS00557; FERM_3; 1.
DR PROSITE; PS0106; PDZ; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
DR Structural protein; Cytoskeleton; Hydrolase.
KW DOMAIN 29 312 FERM.
FT DOMAIN 510 582 PDZ.
FT DOMAIN 670 913 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 842 842 PHOSPHOCYSTEINE INTERMEDIATE
FT (BY SIMILARITY).
SQ SEQUENCE 913 AA; 104029 MW; 29A539ACDE2F1515 CRC64;

Query Match 2.4%; Score 11; DB 1; Length 913;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KRYKDVLPYD 69
Db 673 KRYKDVLPYD 683
|||||
|||||

RESULT 7
ID_PTP3 YEAST STANDARD; PRT; 928 AA.
AC P40048;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase 3 (EC 3.1.3.48) (PTPase 3).
GN PTP3 OR YER075C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OC NCBI_TaxID=4932;
RN Genes Dev. 11:1690-1702(1997).
[1]
SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE=97367951; PubMed=9224718;
Zhan X.-L., Deschenes R.J., Guan K.-L.;
"Differential regulation of FUS3 MAP kinase by tyrosine-specific
phosphatases PTP2/PTP3 and dual-specificity phosphatase MS05 in
Saccharomyces cerevisiae.";
[2]
SEQUENCE FROM N.A.
STRAIN=S288c / AB972;
MEDLINE=97313264; PubMed=9169868;
Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
Araujo R., Aviles E., Berne A., Brennan T., Carpenter J., Chen E.,
Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,
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RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
RL Nature 387:78-81(1997).
CC -!- FUNCTION: Major phosphatase responsible for tyrosine
CC dephosphorylation of MAP kinase FUS3 to inactivate its activity;
CC it also has important roles, along with MS05, in the inactivation
CC of FUS3 following pheromone stimulation.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -!- SIMILARITY: Contains 1 rhodanese domain.
CC
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CC
CC EMBL; AF066304; AAB70811.1; -.
CC EMBL; U18814; AAB64614.1; -.
CC PIR; S50578; S50578.
CC HSP; P29350; 1GWZ.
CC GerMOnline; 139155; -.
CC SGD; S000877; PTP3.
CC GO; GO:0005737; Cytoplasm; IDA.
CC GO; GO:0004725; F:protein tyrosine phosphatase activity; IDA.
CC GO; GO:0000173; P:inactivation of MAPK (osmolality sensing); IMP.
CC GO; GO:0005470; P:protein amino acid dephosphorylation; IDA.
CC GO; GO:0000750; P:signal transduction during conjugation with. .; IMP.
CC InterPro; IPR001763; Rhodanese-like.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; TYR_PP.
CC Pfam; PF00581; Rhodanese; 1.
CC Pfam; PF01102; Y_phosphatase; 1.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00194; PTPC; 1.
CC SMART; SM00450; RHOD; 1.
CC PROSITE; PS00206; RHODANESE_3; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
FT DOMAIN 111 232 RHODANESE.
FT ACT_SITE 804 804 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT DOMAIN 308 311 POLY-SER.
FT DOMAIN 592 597 POLY-THR.
FT DOMAIN 702 715 POLY-ASN.
FT DOMAIN 724 732 POLY-ASP.
SQ SEQUENCE 928 AA; 105250 MW; 6DEC5BA26B7ACBCE CRC64;

Query Match 2.4%; Score 11; DB 1; Length 928;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VHCAGCGRTG 237
Db 802 VHCAGCGRTG 812
|||||
|||||

RESULT 8
ID_PTNE HUMAN STANDARD; PRT; 1187 AA.
AC Q15678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
DE (protein-tyrosine phosphatase pez).
DE
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GN PTPN14 OR PEZ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast carcinoma;
RX MEDLINE=95251727; PubMed=7733990;
RA Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
RT Crompton M.R.;
RT "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and
RL ezrin-like domains.";
RL Biochem. Biophys. Res. Commun. 209:959-965(1995).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- TISSUE SPECIFICITY: Expressed in a variety of human tissues
CC including kidney, skeletal muscle, lung and placenta.
CC -!- SIMILARITY: Contains 1 FERM domain.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X82676; CAA57993.1; -.
CC PIR; JC4155; JC4155.
CC HSSP; P29350; LGW2.
CC Genew; HGNC:9647; PTPN14.
CC MIN; 603155; -.
CC GO; GO:0004725; P:protein tyrosine phosphatase activity; TAS.
CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC InterPro; IPR000299; Band 4.1.
CC InterPro; IPR000387; TYR_Phosphatase.
CC InterPro; IPR000242; Tyr_Pp.
CC Pfam; PF00373; Band_41; 1.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00935; BAND41.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00660; FERM_1; 1.
CC PROSITE; PS00661; FERM_2; 1.
CC PROSITE; PS50057; FERM_3; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_PTP; 1.
CC PROSITE; PS50055; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC structural protein; Cytoskeleton; Hydrolase.
CC FT DOMAIN 21 306 FERM.
CC FT ACT_SITE 1121 1121
CC FT DOMAIN 566 573
CC FT DOMAIN 709 716 POLY-PRO.
CC FT DOMAIN 716 718 POLY-GLU.
CC SEQUENCE 1187 AA; 135239 MW; 015760B75E3574E3 CRC64;

Query Match 2.4%; Score 11; DB 1; Length 1187;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 YIATQGPLEPHT 111
Db 979 YIATQGPLEPHT 989

RESULT 9
PTNE_MOUSE STANDARD; PRT; 1189 AA.
ID PTNE_MOUSE

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AC O62130;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (SC 3.1.3.48)
DE (Protein-tyrosine phosphatase PTP36).
GN PTPN14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB-17-SCID; TISSUE=Thymus;
RX MEDLINE=94354845; PubMed=8074693;
RA Sawada M., Ogata M., Fujino Y., Hamaoka T.;
RT "cDNA cloning of a novel protein tyrosine phosphatase with homology
RT to cytoskeletal protein 4.1 and its expression in T-lineage cells.";
RL Biochem. Biophys. Res. Commun. 203:479-484(1994).
CC -!- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- TISSUE SPECIFICITY: Thymus; in cells of both hematopoietic and
CC non-hematopoietic origins.
CC -!- SIMILARITY: Contains 1 FERM domain.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D31842; BAA06628.1; -.
CC PIR; JC2366; JC2366.
CC HSSP; Q06124; 28HP.
CC MGD; MGI:102467; Ptpn14.
CC InterPro; IPR000299; Band 4.1.
CC InterPro; IPR000387; TYR_Phosphatase.
CC InterPro; IPR000242; Tyr_Pp.
CC Pfam; PF00373; Band_41; 1.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00935; BAND41.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00295; B41; 1.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00660; FERM_1; 1.
CC PROSITE; PS00661; FERM_2; 1.
CC PROSITE; PS50057; FERM_3; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC structural protein; Cytoskeleton; Hydrolase.
CC FT DOMAIN 21 306 FERM.
CC FT DOMAIN 935 1189
CC FT ACT_SITE 1123 1123
CC FT DOMAIN 566 573
CC FT DOMAIN 635 639 POLY-GLY.
CC FT DOMAIN 712 718 POLY-GLU.
CC SEQUENCE 1189 AA; 135030 MW; 2B85B85F9C723303 CRC64;

Query Match 2.4%; Score 11; DB 1; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 YIATQGPLEPHT 111
Db 981 YIATQGPLEPHT 991

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RESULT 10

PTNC_MOUSE STANDARD; PRT; 775 AA.

AC P35831; 2.2%; Score 10; DB 1; Length 775;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-FEB-1996 (Rel. 32, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Protein-tyrosine phosphatase, non-receptor type 12 (EC 3.1.3.48)

DE (Protein-tyrosine phosphatase P19) (P19-PTP) (MPTP-PEST).

GN PTPN12.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RP MEDLINE=92272714; PubMed=1590786;

RX den Hertog J., Pals C.E., Jonk L.J., Kruljg W.;

RA "Differential expression of a novel murine non-receptor protein

RT tyrosine phosphatase during differentiation of F19 embryonal

RT carcinoma cells.";

RT Biochem. Biophys. Res. Commun. 184:1241-1249(1992).

RL [2]

SEQUENCE FROM N.A.

RP MEDLINE=93112015; PubMed=1472029;

RX Takekawa M., Itoh F., Hinoda Y., Arimura Y., Toyota M., Sekiya M.,

RA Adachi M., Imai K., Yachi A.;

RT "Cloning and characterization of a human cDNA encoding a novel

RT putative cytoplasmic protein-tyrosine-phosphatase.";

RL Biochem. Biophys. Res. Commun. 189:1223-1230(1992).

[3]

SEQUENCE FROM N.A.

RP STRAIN=BALB/C;

RX MEDLINE=95289971; PubMed=7772023;

RA Charest A., Wagner J., Shen S.H., Tremblay M.L.;

RT "Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein

RT tyrosine phosphatase.";

RL Biochem. J. 308:425-432(1995).

CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein

CC tyrosine + phosphate.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.

CC Non-receptor class subfamily.

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EMBL; X63440; CAA45037.1; ALT_SEQ.

DR EMBL; X66781; CAA60477.1; -.

DR PIR; S55345; S55345.

DR HSSP; Q06124; 2SHP.

DR MGI; 104673; Ptpn12.

DR InterPro; IPR000387; TYR_phosphatase.

DR InterPro; IPR000242; Tyr_PP.

DR Pfam; PF00102; Y_phosphatase; 1.

DR PRINTS; PR00700; EPTPHPTASE.

DR SMART; SW00194; PTPC; 1.

DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.

DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.

KW Hydrolase.

FT DOMAIN 27 291 PROTEIN-TYROSINE PHOSPHATASE. (BY

FT ACT_SITE 231 PHOSPHOCYSTEINE INTERMEDIATE (BY

FT SIMILARITY).

FT CONFLICT 296 296 K -> N (IN REF. 1).

FT CONFLICT 328 332 KQDSP -> DETS (IN REF. 1).

FT CONFLICT 380 380 W -> V (IN REF. 1).

FT


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GN PTPRN2
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New England Deaconess Hospital; TISSUE=Insulinoma;
RA Wasmeyer C., Hutton J.C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Fitzgerald L.R., Walton K.M., Dixon J.E., Largent B.L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Implicated in development of nervous system and
CC pancreatic endocrine cells.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- PTM: Appears to undergo multiple proteolytic cleavage at
CC consecutive basic residues (By similarity).
CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC
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CC -----
DR EMBL; Z50735; CAA90600.1; -.
DR EMBL; U73458; AAC08036.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTPHPHTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 27
FT CHAIN 28 1004
FT RECEPTOR-TYPE PROTEIN-TYROSINE
FT PHOSPHATASE N2.
FT POTENTIAL.
FT DOMAIN 28 603
FT TRANSMEM 604 624
FT DOMAIN 625 1004
FT DOMAIN 759 993
FT ACT_SITE 934 934
FT SITE 415 416
FT CARBOHYD 553 553
FT N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 1004 AA; 111863 MW; A73929E11B486FB2 CRC64;

Query Match 2.2%; Score 10; DB 1; Length 1004;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 AYIATQGPLP 109
Db 804 AYIATQGPLP 813
|||||
ID_PTPX_MACNE STANDARD; PRT; 1013 AA.
AC O02635;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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DE (R-PTP-N2) (M1851).
DE PTPRN2.
GN Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreatic islets;
RX MEDLINE=97254813; PubMed=9100223;
RA Lagassee P., Jelinek L., Sexson S., Lofton-Day C.E., Breining J.,
RA Sheppard J., Kindsvogel W., Hagopian W.A.;
RT "An islet-cell protein tyrosine phosphatase is a likely precursor to
RT the 37-kDa autoantigen in type 1 diabetes: human and macaque
RT sequences, tissue distribution, unique and shared epitopes, and
RT predictive autoantibodies."
RL Mol. Med. 3:163-173(1997).
CC -!- FUNCTION: Implicated in development of nervous system and
CC pancreatic endocrine cells.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Brain, prostate, pancreatic islets. Lower
CC expression in spinal cord, thyroid, adrenal medulla and
CC gastrointestinal tract.
CC -!- PTM: Appears to undergo multiple proteolytic cleavage at
CC consecutive basic residues (By similarity).
CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC
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CC -----
DR EMBL; U91574; AAC51186.1; -.
DR HSSP; P18052; 1YFO.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTPHPHTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane.
FT SIGNAL 1 19
FT CHAIN 20 1013
FT RECEPTOR-TYPE PROTEIN-TYROSINE
FT PHOSPHATASE N2.
FT POTENTIAL.
FT DOMAIN 20 613
FT TRANSMEM 614 634
FT DOMAIN 635 1013
FT DOMAIN 768 1002
FT ACT_SITE 943 943
FT SITE 425 426
FT CARBOHYD 562 562
FT N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 1013 AA; 111190 MW; 4808D43937A2EF59 CRC64;

Query Match 2.2%; Score 10; DB 1; Length 1013;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 AYIATQGPLP 109
Db 813 AYIATQGPLP 822
|||||
RESULT 15
PTPX_HUMAN

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ID AC 092932; Q8N415; Q92662; PRT; 1015 AA.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-NOV-1997 (Rel. 35, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Receptor-type protein-tyrosine phosphatase N2 precursor (BC 3.1.3.48)
DE (R-PTP-N2) (Islet cell autoantigen related protein) (ICAP) (IAR)
DE (Phogrin).
DE (Phogrin).
GN PTPN22.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Pancreas;
RX MEDLINE=97032784; PubMed=8878534;
RA Kawasaki E., Hutton J.C., Eisenbarth G.S.;
RT "Molecular cloning and characterization of the human transmembrane
RT protein tyrosine phosphatase homologue, phogrin, an autoantigen of
RT type 1 diabetes.";
RL Biochem. Biophys. Res. Commun. 227:440-447(1996).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Fetal brain;
RX MEDLINE=97127415; PubMed=8954911;
RA Smith P.D., Barker K.T., Wang J., Lu Y.-J., Shipley J., Crompton M.R.;
RT "ICAPAR, a novel member of a new family of transmembrane, tyrosine
RT phosphatase-like proteins.";
RL Biochem. Biophys. Res. Commun. 229:402-411(1996).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain and Pancreas;
RX MEDLINE=96394649; PubMed=7897855;
RA Cui L., Xu W.-P., de Azavedo H.J., Schmidl R.S., Pallen C.J.;
RT "Cloning and characterization of islet cell antigen-related protein-
RT tyrosine phosphatase (PTP), a novel
RT in insulin-dependent diabetes.";
RL J. Biol. Chem. 271:24817-24823(1996).
[4]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Implicated in development of nervous system and
CC pancreatic endocrine cells.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q92932-1; Sequence=Displayed;
CC Name=2;

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CC IsoId=Q92932-2; Sequence=VSP_007779;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Highest levels in brain and pancreas. Lower
CC levels in trachea, prostate, stomach and spinal chord.
CC -!- DOMAIN: The cytoplasmic domain appears to contain the
CC autoantigenic epitopes.
CC -!- PTM: Appears to undergo multiple proteolytic cleavage at
CC consecutive basic residues.
CC -!- DISEASE: Autoantigen in insulin-dependent diabetes mellitus
CC (IDDM).
CC -!- MISCELLANEOUS: Optimum activity is measured at pH 4.5.
CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC -----
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CC -----
CC EMBL; U66702; AAC50742.1; -;
CC EMBL; Y08569; CAA69880.1; -;
CC EMBL; AF007555; AAB63600.1; -;
CC EMBL; BC034040; AAH34040.1; -;
CC PIR; JC5062; JC5062.
CC PIR; JC5263; JC5263.
CC HSP; P18052; LYFO.
CC Genew; HGNC:9677; PTPN22.
CC MIM; 601698; -;
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC GO; GO:0005001; P: transmembrane receptor protein tyrosine pho. .; TAS.
CC GO; GO:0006470; P: protein amino acid dephosphorylation; TAS.
CC InterPro; IPR003595; PTPC motif.
CC InterPro; IPR000387; Tyr_P.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00700; PTPHPHTASE.
CC SMART; SM00194; PTPC; 1.
CC SMART; SM00404; PTPC motif; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
CC Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
CC Diabetes mellitus; Alternative splicing.
CC SIGNAL 1 21
CC CHAIN 22 1015
CC RECEPTOR-TYPE PROTEIN-TYROSINE
CC PHOSPHATASE N2.
CC EXTRACELLULAR (POTENTIAL).
CC POTENTIAL.
CC CYTOPLASMIC (POTENTIAL).
CC PROTEIN-TYROSINE PHOSPHATASE.
CC PHOSPHOCYSTEINE INTERMEDIATE (BY
CC SIMILARITY).
CC CLEAVAGE SITE (POTENTIAL).
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC Missing (in isoform 2).
CC /FTID=VSP_007779.
CC C->S: LOSS OF ACTIVITY.
CC P -> S (IN REF. 2 AND 3).
CC S -> G (IN REF. 2).
CC G -> R (IN REF. 2).
CC S -> N (IN REF. 2).
CC S -> N (IN REF. 2).
CC SEQUENCE 1015 AA; 111281 MW; 82AC3C9F59A6C97 CRC64;

```

Query Match 2.2%; Score 10; DB 1; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AYIATQGLP 109
 |||||
 DB 815 AYIATQGLP 824

Search completed: August 17, 2004, 20:50:34
Job time : 20 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:48:22 ; Search time 44 Seconds
(without alignments)

3284.258 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 458
Sequence: 1 MSRLSDARSFLERLEARGG.....NLIRGPKGRDPPAEWTRV 458

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: SPTEMBL 25:*

1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_nhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	47.4	351	4 Q72637	Q72637 homo sapien
2	217	47.4	372	4 Q8TA96	Q8TA96 homo sapien
3	32	7.0	453	11 Q922E3	Q922E3 mus musculus
4	32	7.0	453	11 Q611S2	Q611S2 mus musculus
5	29	6.3	453	11 P70602	P70602 rattus norv
6	12	2.6	258	13 Q90Y62	Q90Y62 brachydanio
7	12	2.6	487	5 Q9NL13	Q9NL13 brachyosteo
8	11	2.4	84	4 Q93095	Q93095 homo sapien
9	11	2.4	292	4 Q8N4S3	Q8N4S3 homo sapien
10	11	2.4	471	5 Q9Y1X6	Q9Y1X6 ephydaria f
11	11	2.4	799	4 Q9P0U2	Q9P0U2 homo sapien
12	11	2.4	802	11 Q7TMP9	Q7TMP9 mus musculus
13	11	2.4	849	11 Q9JLJ8	Q9JLJ8 mus musculus
14	11	2.4	1104	3 Q9P664	Q9P664 neurospora
15	10	2.2	248	4 Q9NSR5	Q9NSR5 homo sapien
16	10	2.2	340	10 Q6S190	Q6S190 arabidopsis

17	10	2.2	340	10	Q82656	Q82656 arabidopsis
18	10	2.2	382	11	Q63745	Q63745 rattus norv
19	10	2.2	438	11	Q64642	Q64642 rattus norv
20	10	2.2	508	13	Q90Y75	Q90Y75 brachydanio
21	10	2.2	582	11	Q64896	Q64896 mus musculus
22	10	2.2	597	13	Q91871	Q91871 xenopus lae
23	10	2.2	694	13	Q91870	Q91870 xenopus lae
24	10	2.2	694	13	Q7ZYN2	Q7ZYN2 xenopus lae
25	10	2.2	775	11	Q80UM4	Q80UM4 mus musculus
26	10	2.2	857	13	Q90YJ4	Q90YJ4 brachydanio
27	10	2.2	872	4	Q86XU4	Q86XU4 homo sapien
28	10	2.2	986	4	Q9Y4I9	Q9Y4I9 homo sapien
29	10	2.2	998	4	Q9Y4I6	Q9Y4I6 homo sapien
30	10	2.2	1042	4	Q9Y4F8	Q9Y4F8 homo sapien
31	10	2.2	1191	4	Q7Z3X4	Q7Z3X4 homo sapien
32	10	2.2	1399	4	Q75870	Q75870 homo sapien
33	10	2.2	1437	5	Q44329	Q44329 hirudo medi
34	10	2.2	1499	13	Q90815	Q90815 gallus gall
35	10	2.2	1501	11	Q9QW00	Q9QW00 rattus sp.
36	10	2.2	1501	11	Q7TTL7	Q7TTL7 mus musculus
37	10	2.2	1502	4	Q9UM81	Q9UM81 homo sapien
38	10	2.2	1788	13	Q9IAJ0	Q9IAJ0 xenopus lae
39	10	2.2	1863	11	Q64605	Q64605 rattus norv
40	10	2.2	1887	11	Q9QW67	Q9QW67 rattus sp.
41	10	2.2	1896	13	Q9IAJ1	Q9IAJ1 xenopus lae
42	10	2.2	1898	11	Q9EQ17	Q9EQ17 mus musculus
43	10	2.2	1898	11	Q64604	Q64604 r protein-t
44	10	2.2	1904	11	Q64699	Q64699 mus musculus
45	10	2.2	2051	5	Q44328	Q44328 hirudo medi

ALIGNMENTS

RESULT 1

Q72637 PRELIMINARY; PRT; 351 AA.
ID Q72637
AC Q72637
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE PTPN18 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lottuallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griewood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Krzywicki M.I., Skalska U., Small D.E., Scherch A., Schain J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;

RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052800; AAH52800.1; -.
SQ SEQUENCE 351 AA; 38317 MW; 5FE9B48C5D0667C4 CRC64;

Query Match 47.4%; Score 217; DB 4; Length 351;
Best Local Similarity 100.0%; Pred. No. 5.2e-213;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 KRCERYWAQOEPLQTLGFCITLKEKWLNEIMRLTKVTFKESRSVYQLYMSWPD 198
DB |||||
QY 32 KRCERYWAQOEPLQTLGFCITLKEKWLNEIMRLTKVTFKESRSVYQLYMSWPD 91
DB |||||
QY 199 GVPSSPDHMLAWBEARRLQSGPEPLCVHCSAGCGRTGVLCTVDYVYRQLLTQMIPDP 258
DB |||||
QY 92 GVPSSPDHMLAWBEARRLQSGPEPLCVHCSAGCGRTGVLCTVDYVYRQLLTQMIPDP 151
DB |||||
QY 259 SLFDVVLKMRKORPAAVQTEQYRFLYHTVAQMFCSLQNASPHYQNIKENCAPLYDDAL 318
DB |||||
QY 152 SLFDVVLKMRKORPAAVQTEQYRFLYHTVAQMFCSLQNASPHYQNIKENCAPLYDDAL 211
DB |||||
QY 319 FLRTPQALLAIPRPPGGVLRISVPGSPGHAMADTYA 355
DB |||||
QY 212 FLRTPQALLAIPRPPGGVLRISVPGSPGHAMADTYA 248
DB |||||

RESULT 2

ID Q8TA96 PRELIMINARY; PRT; 372 AA.
AC Q8TA96;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to protein tyrosine phosphatase, non-receptor type 18
DE (Brain-derived) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024280; AAH24280.1; -.
DR EMBL; BC041562; AAH41562.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_Pp.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_ptp; 1.
KW Hydrolase; Receptor.
FT NON TR 1
SQ SEQUENCE 372 AA; 40708 MW; 417CA80AA054CF8B CRC64;

Query Match 47.4%; Score 217; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 5.4e-213;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 KRCERYWAQOEPLQTLGFCITLKEKWLNEIMRLTKVTFKESRSVYQLYMSWPD 198
DB |||||
QY 53 KRCERYWAQOEPLQTLGFCITLKEKWLNEIMRLTKVTFKESRSVYQLYMSWPD 112
DB |||||
QY 199 GVPSSPDHMLAWBEARRLQSGPEPLCVHCSAGCGRTGVLCTVDYVYRQLLTQMIPDP 258
DB |||||
QY 113 GVPSSPDHMLAWBEARRLQSGPEPLCVHCSAGCGRTGVLCTVDYVYRQLLTQMIPDP 172
DB |||||

Query Match 47.4%; Score 217; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 5.4e-213;
Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 SLFDVVLKMRKORPAAVQTEQYRFLYHTVAQMFCSLQNASPHYQNIKENCAPLYDDAL 318
DB |||||
QY 173 SLFDVVLKMRKORPAAVQTEQYRFLYHTVAQMFCSLQNASPHYQNIKENCAPLYDDAL 232
DB |||||
QY 319 FLRTPQALLAIPRPPGGVLRISVPGSPGHAMADTYA 355
DB |||||
QY 233 FLRTPQALLAIPRPPGGVLRISVPGSPGHAMADTYA 269
DB |||||

RESULT 3

ID Q922E3 PRELIMINARY; PRT; 453 AA.
AC Q922E3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to protein tyrosine phosphatase, non-receptor type 18.
DE PTPN18.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008512; AAH08512.1; -.
DR MGD; MGI:108410; Ptpn18.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phosphatase.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_Pp.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_ptp; 1.
KW Hydrolase; Receptor.
SQ SEQUENCE 453 AA; 50227 MW; 722FDE1FFC9F4689 CRC64;

Query Match 7.0%; Score 32; DB 11; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AYIATQGPLPHTLLDFWELVWFGVKVLMAC 131
DB |||||
QY 100 AYIATQGPLPHTLLDFWELVWFGVKVLMAC 131
DB |||||

RESULT 4

ID Q61152 PRELIMINARY; PRT; 453 AA.
AC Q61152; Q62404;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (PTP-K1) (Fetal liver phosphatase 1) (FLP1) (PTP 49) (PTP HSCF).
GN PTPN18 OR PTPK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RA Cheng J., Daimaru L., Fennie C., Lasky L.A.;
RT "A novel protein tyrosine phosphatase expressed in lin(10)CD34(hi)Sca(hi) hematopoietic progenitor cells.";
RX MEDLINE=96329547; PubMed=8698932;
RN TISSUE=EMERYO;
RP SEQUENCE FROM N.A.

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RL Blood 88:1156-1167(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=97030045; PubMed=8875997;
RA Huang K., Sommers C.L., Grinberg A., Kozak C.A., Love P.E.;
RT "Cloning and characterization of PTP-Ki, a novel nonreceptor protein
RL tyrosine phosphatase highly expressed in bone marrow.";
RL Oncogene 13:1567-1573(1996).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=C57BL/6; TISSUE=FETAL LIVER;
RX MEDLINE=97131769; PubMed=977243;
RA Dosil M., Leibman N., Lemischka I.R.;
RT "Cloning and characterization of fetal liver phosphatase 1, a nuclear
RL protein tyrosine phosphatase isolated from hematopoietic stem cells.";
RL Blood 88:4510-4525(1996).
CC -!- FUNCTION: MAY BE INVOLVED IN GROWTH AND DIFFERENTIATION OF
CC HEMATOPOIETIC CELLS.
CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN
CC TYROSINE + PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=FLPIA;
CC IsoId=061152-1; Sequence=Displayed;
CC Name=FLPIB;
CC IsoId=061152-2; Sequence=VSP_050405;
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BONE MARROW. ALSO
CC EXPRESSED IN KIDNEY, LUNG, OVARY, SPLEEN, THYMUS AND LYMPH NODE.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 15.5.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
DR EMBL; U35124; AB82736.1; -.
DR EMBL; U49853; AB18623.1; -.
DR EMBL; U52523; AAC52991.1; -.
DR HSSP; Q06124; 2SHP.
DR MGD; MGI:108410; Ptpn18.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . . ; IDA.
DR InterPro; IPR000387; Tyr_PP.
DR InterPro; IPR00242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR DOMAIN 56 PROTEIN-TYROSINE PHOSPHATASE.
DR DOMAIN 312 428 PRO/SER/THR-RICH.
DR ACT_SITE 229 229 BY SIMILARITY.
DR VARSPIC 9 32 Missing (in isoform FLPIB).
DR FT FTId=VSP_050405.
DR FT CONFLICT 11 11 F -> L (IN REF. 3).
DR FT CONFLICT 362 368 ASATGP -> LRHRA (IN REF. 3).
SQ SEQUENCE 453 AA; 50201 MW; 88AD7E73CE8136B0 CRC64;

Query Match 7.0%; Score 32; DB 11; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AYIATQGPLPHTLLDFWELVWFGVKVILMAC 131
D5 100 AYIATQGPLPHTLLDFWELVWFGVKVILMAC 131

RESULT 5
P70602
ID P70602 PRELIMINARY; PRT; 453 AA.
AC P70602;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)

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DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protein tyrosine phosphatase 20.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97067206; PubMed=8910608;
RA Aoki N., Yamaguchi-Aoki Y., Ullrich A.;
RT "The novel protein-tyrosine phosphatase PTP20 is a positive regulator
of PC12 cell neuronal differentiation.";
RL J. Biol. Chem. 271:29422-29426(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Aoki N., Yamaguchi-Aoki Y., Ullrich A.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U69673; AAC52896.1; -.
DR HSSP; Q06124; 2SHP.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR Hydrolase.
KW HYDROLASE.
SQ SEQUENCE 453 AA; 50106 MW; 6CCC132206FB69AE CRC64;

Query Match 6.3%; Score 29; DB 11; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 GAQTGGLGNLRIGRPKGRPPPAEWTRV 458
D5 425 GAQTGGLGNLRIGRPKGRPPPAEWTRV 453

RESULT 6
Q90Y62
ID Q90Y62 PRELIMINARY; PRT; 258 AA.
AC Q90Y62;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Receptor PTP-like protein IA-2 (Fragment).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21076097; PubMed=11206415;
RA Cai T., Krause M.W., Odenwald W.F., Toyama R., Notkins A.L.;
RT "The IA-2 gene family: homologs in Caenorhabditis elegans, Drosophila
and zebrafish.";
RL Diabetologia 44:81-88(2001).
DR EMBL; AF190144; AAL05974.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.

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DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolyase.
FT NON TER
SQ SEQUENCE 258 AA; 29544 MW; 93FBC53CAA4EAA2 CRC64;
Query Match 2.6%; Score 12; DB 13; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 100 AYIATQGLPHT 111
Db 58 AYIATQGLPHT 69
RESULT 7
ID Q9NL13 PRELIMINARY; PRT; 487 AA.
AC Q9NL13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AMTPR4C protein (Fragment).
GN AMTPR4C.
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;
RA Ono-Koyanagi K., Suga H., Katoh K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RL J. Mol. Evol. 50:302-311 (2000).
DR EMBL; AB033564; BAA95171.1; -.
DR HSSP; P18052; 1YFO.
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolyase.
FT NON TER
SQ SEQUENCE 487 AA; 55573 MW; CF2BCC6D933C6ADD CRC64;
Query Match 2.6%; Score 12; DB 5; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 100 AYIATQGLPHT 111
Db 267 AYIATQGLPHT 278
RESULT 8
ID Q93095 PRELIMINARY; PRT; 84 AA.
AC Q93095;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protein tyrosine phosphatase PEP (EC 3.1.3.48) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dayton M.A., Knudloch T.J.;
RT "Multiple phosphotyrosine phosphatase mRNAs are expressed in the human
RT lung fibroblast cell line WI-38.";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U69700; AAB09079.1; -.
DR HSSP; P29350; 1GWZ.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004727; F:phosphorylated protein tyrosine phosphatase act. .; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolyase.
FT NON TER
SQ SEQUENCE 84 AA; 9699 MW; 4DA40B7BA38E45DA CRC64;
Query Match 2.4%; Score 11; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 228 HCSAGCGRTGV 238
Db 67 HCSAGCGRTGV 77
RESULT 9
ID Q8N4S3 PRELIMINARY; PRT; 292 AA.
AC Q8N4S3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Renal adenocarcinoma;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC033716; AAH33716.1; -.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC motif; 1.
DR PROSITE; PS00215; MITOCH CARRIER; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 292 AA; 33121 MW; 54B838BDD41D1BD7 CRC64;
Query Match 2.4%; Score 11; DB 4; Length 292;

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Best Local Similarity 100.0%; Pred. No. 0.027; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 KNRYKDVLPYD 69
Dd 52 KNRYKDVLPYD 62

RESULT 10

ID Q9YIX6 PRELIMINARY; PRT; 471 AA.
AC Q9YIX6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SPTRF4 (Fragment);
OS Ephydatia fluviatilis.
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Haploclerida; Spongillidae; Ephydatia.
OX NCBI_TaxID=31330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9246376; PubMed=1029569;
RA Ono K., Suga H., Iwabe N., Kuma K., Miyata T.;
RT "Multiple protein tyrosine phosphatases in sponges and explosive gene
RT duplication in the early evolution of animals before the parazoan-
RT eumetazoan split.";
EL J. Mol. Evol. 48:654-662(1999).
DR EMBL; AB019125; BAA82558.1; -.
DR HSSP; P18052; IYFO.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS0056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER 1 1
SQ SEQUENCE 471 AA; 54509 MW; 7DA6245615A46A56 CRC64;

Query Match 2.4%; Score 11; DB 5; Length 471;
Best Local Similarity 100.0%; Pred. No. 0.042; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCAGCGRTG 237
Dd 399 VHCAGCGRTG 409

RESULT 11

ID Q9POU2 PRELIMINARY; PRT; 799 AA.
AC Q9POU2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protein tyrosine phosphatase.
GN PTP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RA Huang C., Zhang C., Wu T., Peng Y., Gu Y., Zhang L., Jiang C., Li Y.,
RA Han Z., Wang Y., Chen Z., Fu G.;
RT "A novel gene expressed in human adrenal gland.";

Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AF150732; AAF67472.1; -.
DR HSSP; P29350; IGMZ.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 799 AA; 90610 MW; 93F5385016F33D0C CRC64;

Query Match 2.4%; Score 11; DB 4; Length 799;
Best Local Similarity 100.0%; Pred. No. 0.067; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 228 HCSAGCGRTG 238
Dd 226 HCSAGCGRTG 236

RESULT 12

ID Q7TMP9 PRELIMINARY; PRT; 802 AA.
AC Q7TMP9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
EX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055377; AAH55377.1; -.
KW Receptor.
SQ SEQUENCE 802 AA; 89694 MW; BB8C3AA618B28561 CRC64;

Query Match 2.4%; Score 11; DB 11; Length 802;
Best Local Similarity 100.0%; Pred. No. 0.067;


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DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.  
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.  
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.  
KW Hypothetical protein; Hydrolase.  
FT NON TER 1  
SQ SEQUENCE 248 AA; 28304 MW; EE10C57EBC5B5114 CRC64;  
  
Query Match 2.28; Score 10; DB 4; Length 248;  
Best Local Similarity 100.0%; Pred.No. 0.25;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Sequence 16, Appl
Sequence 37, Appl
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Sequence 19, Appl
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Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl

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29 448.5 18.5 232 2 US-08-446-345-38
30 448 18.5 913 4 US-09-848-294-2
31 441.5 18.2 242 2 US-08-685-992-21
32 441.5 18.2 242 2 US-09-144-925-21
33 435 17.9 1337 3 US-08-854-585-2
34 435 17.9 1337 4 US-09-447-533-2
35 435 17.9 1337 5 PCT-US95-05512-2
36 433 17.9 274 4 US-08-848-294-7
37 429.5 17.7 278 1 US-08-201-697-16
38 429 17.7 231 2 US-08-446-345-37
39 426.5 17.6 802 1 US-08-015-985-1
40 426.5 17.6 802 4 US-09-280-537-1
41 426 17.6 258 2 US-08-685-992-19
42 426 17.6 258 2 US-09-144-925-19
43 424.5 17.5 385 1 US-08-036-210-5
44 424.5 17.5 385 2 US-08-449-609-5
45 424.5 17.5 385 4 US-09-361-096A-5

ALIGNMENTS

RESULT 1

US-08-821-278A-2
; Sequence 2, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 2
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Mus Musculus
US-08-821-278A-2

Query Match 73.4%; Score 1778.5; DB 3; Length 453;
Best Local Similarity 74.9%; Pred. NO. 7.9e-154;
Matches 344; Conservative 32; Mismatches 76; Indels 7; Gaps 2;

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DB 1 MSRLDLSRSLERLEARGGREGVLAAGEFSDIQAASAADKAGVCSVTAGSRPENVRKN 60
QY 61 RYKDVLPYDQTRVILSLQEEHSDYINGNFIRGVDSLAYIATQGPLPHTLLDFWRLVW 120
DB 61 RYKDVVAYDETRVILSLQEEHSDYINGNFIRGVDSLAYIATQGPLPHTLLDFWRLVW 120
QY 121 EFGVKVILMACREIENGRCERYWAQCEPLQGLFCITLIKKEWLNEDIMRLTKYTF 180
DB 121 EFGVKVILMACREIENGRCERYWAQCEPLQGLFCITLIKKEWLNEDIMRLTKYTF 180
QY 181 QKESRSVYQLOQYMSWPDGVPSSPDHMLAMVEEARLQSGPEPLCHVCSAGCGRTGVLIC 240
DB 181 QKESRSVYQLOQYMSWPDGVPSSPDHMLAMVEEARLQSGPEPLCHVCSAGCGRTGVLIC 240
QY 241 TVDYVRQLLLTQMIPDFSLFDVILKMKQKPAAVQTEQYRFLYHTVAQFCSLTQNAS 300
DB 241 AVDYVRQLLLTQMIPDFSLFDVILKMKQKPAAVQTEQYRFLYHTVAQFCSLTQNAS 300
QY 301 PHYQNKENCAPLYDDALFLRTPQALLAIPRPPGGVLSISVPGSPGHAMADTYAEOKR 360
DB 301 PHYQNKENCAPLYDDALFLRTPQALLAIPRPPGGVLSISVPGSPGHAMADTYAEOKR 360
QY 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTPRAQPGAHAEADAGTLP-GRVPAQDQSPA 419
DB 361 GASAGTGPGRAPTST-----DTPYISQVAPRAQRPVAHTEDAQGTTLALRRVPADONSS 414

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1778.5	73.4	453	3	US-08-821-278A-2
2	1754.5	72.4	453	3	US-08-951-260A-7
3	1754.5	72.4	453	4	US-08-430-626A-7
4	830	34.2	155	3	US-08-821-278A-17
5	755.5	31.2	802	3	US-08-081-345-18
6	727.5	30.0	807	3	US-08-081-345-2
7	715.5	29.5	278	3	US-08-821-278A-18
8	695	28.7	272	3	US-08-821-278A-19
9	665	27.4	253	2	US-08-685-992-20
10	665	27.4	253	2	US-08-144-925-20
11	493.5	20.4	255	2	US-08-685-992-16
12	493.5	20.4	255	2	US-08-144-925-16
13	474	19.6	1711	2	US-08-342-930-2
14	467	19.3	595	1	US-08-202-389-6
15	465	19.2	631	1	US-08-202-389-8
16	463.5	19.1	277	2	US-08-685-992-22
17	463.5	19.1	277	2	US-08-144-925-22
18	463.5	19.1	513	1	US-08-202-389-2
19	463	19.1	843	4	US-09-417-197-117
20	463	19.1	853	4	US-09-417-197-119
21	461	19.0	593	1	US-08-018-129-5
22	461	19.0	593	4	US-08-448-250-5
23	461	19.0	593	4	US-09-282-257-5
24	456	18.8	263	2	US-08-685-992-13
25	456	18.8	263	2	US-09-144-925-13
26	454	18.7	266	2	US-08-685-992-12
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Best Local Similarity 74.5%; Pred. No. 1.2e-151;
Matches 342; Conservative 37; Mismatches 73; Indels 7; Gaps 3;

Qy 1 MSRLDARGFLERLEARGREGAVLAGESFDIOACSAAMKADGVCSTVAGSPENVRKN 60
Db 1 MSQSDLVRFLEQOEARDHRKGAILEAFESDIKARSAWKTGVCSTAGSQGSKN 60
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Db 61 RYKDVLPYDQTRVLSLLQEGHSDYINGNPIRGVDSGLAYIATQGPLPHTLLDFWRLV 120
Qy 121 EFGVKVILMACRETEGRKCECERWAOEPLQTGLFCITLKEKWLNEDIMLTKVTF 180
Db 121 EFGKIVILMACQETENGRRCERWAOERPLQAGPFCITLTRETAITSITRTIQTQVF 180
Qy 181 QKESRSYQLYQSWPDRGVPSPDHMLAMVEARLQSGPPEPLCVHCSAGCGRTGVLC 240
Db 181 QKESRPVHQLYQSWPDHGVSPSSDHLITWVEARCLQGLGPGPLCVHCSAGCGRTGVLC 240
Qy 241 TVDYVROLITQMIPTDFSLFDVVLKVRKORPAAVQTEEQRYFLYHTVAQMFCSSTLONAS 300
Db 241 AVDYVROLITQMIPTDFSLFDVVLKVRKORPAAVQTEEQRYFLYHTVAQMFCSSTLONAS 300
Qy 301 PHYNIKENCAPLYDDALFRTPCALLAI PRPPGGVLRSTSVPGSPGHAMADTYAEQKR 360
Db 301 FLVQLKENCAPICKSSSLRTSALPATSRPIGGVLRSTSVPGPPTLPMADTYAVVQKR 360
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Db 361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTEAQAQTALGRVPADENPS 414
Qy 420 GSGAYEDVAGGAOTGGGLENLRIGRPGKPRDPAETRV 458
Db 415 GPDAIEVTDQATGGGLGFNLRIGRPKGPRDPAETRV 453

RESULT 4
US-08-821-278A-17
; Sequence 17, Application US/08821278A
; Patent No. 6238502
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 17
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo Sapien
US-08-821-278A-17

Query Match 34.2%; Score 830; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.5e-68;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 ARGREGAVLAGESFDIOACSAAMKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVLS 76
Db 1 ARGREGAVLAGESFDIOACSAAMKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVLS 60
Qy 77 LLOEGHSDYINGNPIRGVDSGLAYIATQGPLPHTLLDFWRLVWFGVKVILMACREIEN 136
Db 61 LLOEGHSDYINGNPIRGVDSGLAYIATQGPLPHTLLDFWRLVWFGVKVILMACREIEN 120
Qy 137 GRKRCERYWAOEPLQTGLFCITLKEKWLNEDI 171
Db 121 GRKRCERYWAOEPLQTGLFCITLKEKWLNEDI 155

RESULT 5
US-09-081-345-18
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; Sequence 18, Application US/09081345
; Patent No. 6228641
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: PTP04 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,345
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/047,222
; FILING DATE: May 20, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/253
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 802 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-081-345-18

Query Match 31.2%; Score 755.5; DB 3; Length 802;
Best Local Similarity 44.0%; Pred. No. 3.6e-60;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;

Qy 27 AGEPSDIOACSAAMKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVLSLLQEGHSDY 86
Db 25 ASEFLKLRQSTKYKADKIYTTVAQRPNKIKKRYKDIILPYDHSLSLTTSDSSY 84
Qy 87 INGNPIRGVDSGLAYIATQGPLPHTLLDFWRLVWFGVKVILMACREIENGRKRCERYWA 146
Db 85 INASPIKGYGPKAYIATQGPLSTLLDFWRLVWFGVKVILMACREIENGRKRCERYWA 144
Qy 147 QEOR-PLQTGLFCITLKEKWLNEDIMLTKVTFQKESRSVYQLYQSWPDRGVPSSPD 205
Db 145 EPGETQLQGFQSPFSCEAEK-KKSDYKIRTLKAKFNNEIRIYQHYKNWPDHDPSSID 203
Qy 206 HMLAMVEARLQSGPPEPLCVHCSAGCGRTGVLCITVDYVRLQILLTQMIPTDFSLFDVYL 265
Db 204 PLQLIWMRCYQEDDDCVPICHCSAGCGRTGVCAVDYTWMLLKDGIIIPKFNFSVENLIQ 263
Qy 266 KVRKORPAAVQTEEQRYFLYHTVAQMFCSSTLONASPHYQNIKENCAPLYDDALFLRTQA 325
Db 264 EMRTORPSLVQTEQRYFLYHTVAQMFCSSTLONASPHYQNIKENCAPLYDDALFLRTQA 308
Qy 326 LLAIRPPFGVLRSTSVPGS-----PGHAMAD--TVAEOKRGAPAGAGSGTGTGTG 377
Db 309 QCSIFE-----QSLTVEADSCPLDLPKVAERDVKTINQHSKQGAESSTGSSLSGLRTS 362
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QY 378 ARSAEE 383
Db 363 TMAEE 368

RESULT 6

US-09-081-345-2
; Sequence 2, Application US/09081345
; Patent No. 6228641
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; APPLICANT: Gregory D. Plowman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: PTPO4 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,345
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/047,222
; FILING DATE: May 20, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/253
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-081-345-2

Query Match 30.0%; Score 727.5; DB 3; Length 807;
Best Local Similarity 46.9%; Pred. No. 1.3e-57;
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;
QY 27 AGEFSDIQACSAANKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVILSLLOEGHSDY 86
Db 25 ANEFLKLRQSTKYKADKTYPTTVAQRPKNIKKNRYKDVLPYDQTRVILSLTSDSDSY 84
QY 87 INGNFIRGVDGSLAYIATQGPLHTLLDFWRLVWFEFGVKVILMACREIENGRKRCERYWA 146
Db 85 INANFIKGVGPKAYIATQGPLSTLLDFWRMIWEYSVLIIVMACMEYEMGKKKERYWA 144
QY 147 QEQP-PLQTGLFCITLKEKWLNEIMRLTKVTFQKESRSVYQLOQYMSWPDGVPSSPD 205
Db 145 EPGEMQLEFGFPFSSCAAEK-RKSDYIIRTLKVKFNSETETIYQFHYKNWPDHVPSSID 203
QY 206 HMLAMVEARLQSGPEPLCVHCSAGCGRTGVLTVDYVRQLLTQMIIPDPSLFDVVL 265
Db 204 PILELINDVRCYQEDDSDVPICHCACCGRTGVICAIDYTWMLLDKGIIPENFSVFLIR 263

QY 266 KMRKQRPAAVQTERQYRFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
Db 264 EMRTQPSLVQTSQYELVYNVLELFRQMDVIRDKHSGTESQAKHCIP 313

RESULT 7

US-08-821-278A-18
; Sequence 18, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-08-821-278A-18

Query Match 29.5%; Score 715.5; DB 3; Length 278;
Best Local Similarity 48.9%; Pred. No. 3.5e-57;
Matches 139; Conservative 45; Mismatches 91; Indels 9; Gaps 3;
QY 27 AGEFSDIQACSAANKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVILSLLOEGHSDY 86
Db 2 ASEFLKLRQSTKYKADKTYPTTVAQRPKNIKKNRYKDVLPYDQTRVILSLTSDSDSY 61
QY 87 INGNFIRGVDGSLAYIATQGPLHTLLDFWRLVWFEFGVKVILMACREIENGRKRCERYWA 146
Db 62 INASFIKGVGPKAYIATQGPLSTLLDFWRMIWEYSVLIIVMACMEYEMGKKKERYWA 121
QY 147 QEQP-PLQTGLFCITLKEKWLNEIMRLTKVTFQKESRSVYQLOQYMSWPDGVPSSPD 205
Db 122 EPGEMQLEFGFPFSSCAAEK-KKSDYKIRTLKAKFNNEITRIYQFHYKNWPDHVPSSID 180
QY 206 HMLAMVEARLQSGPEPLCVHCSAGCGRTGVLTVDYVRQLLTQMIIPDPSLFDVVL 265
Db 181 PILELINDVRCYQEDDSDVPICHCACCGRTGVICAIDYTWMLLDKGIIPENFSVFLIR 240
QY 266 KMRKQRPAAVQTERQYRFLYHTVAQMFCSLTQNASPHYQNIKEN 309
Db 241 EMRTQPSLVQTSQYELVYNVLELFRQMDVIRDKHSGTESQAKHCIP 313

RESULT 8

US-08-821-278A-19
; Sequence 19, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 19
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo Sapien
US-08-821-278A-19

Query Match 28.7%; Score 695; DB 3; Length 272;
Best Local Similarity 47.1%; Pred. No. 2.5e-57;
Matches 128; Conservative 55; Mismatches 87; Indels 2; Gaps 2;
QY 27 AGEFSDIQACSAANKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVILSLLOEGHSDY 86
Db 25 ANEFLKLRQSTKYKADKTYPTTVAQRPKNIKKNRYKDVLPYDQTRVILSLTSDSDSY 84

Db 2 ARDFWRLRLSTKYRTEKIYPTATGEKEENVKKNRYKDILPFDHRSRVKLTLPKTPSQSDY 61
 QY 97 INGNFIRGVDGLSLAYIATQGLPHLLDFWRLVWFGVKVILMACREIENGRKRCERYW- 145
 Db 62 INANFIKGVGPKAYVATQGLANTVIDFWMVWYNNVWIIVMACREFEMGRKKCERYP 121
 QY 146 AQEQEPQTLGFCITLILKEKWLNEIDIMRLTKVTFOKESRVYQLQYMSWPDGRGVSSPD 205
 Db 122 LYGEDPITFAFKLS-CEDEQARTDYFIRITLLLEFQNESRRLYQFHYVNNPDDHVPSSFD 180
 QY 206 HMLAMVEARLQSGPEPLCVHCSAGCGRTGLVCTVDYVROLTLTQMIPPDFSLEFDVVL 265
 Db 181 SILDMISLMRYQEHEDVPICIHCSAGCGRTGAICAIDYTNLLKAGKIPEEFNVNLIQ 240
 QY 266 KRRQORPAAVQTERQYRFLVHTVAQMFCSLQ 297
 Db 241 EMRTORHSAVQTEQYELVHRAIAQLFEKQLQ 272

RESULT 9
 US-08-685-992-20
 ; Sequence 20, Application US/08685992
 ; Patent No. 5912138
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas
 ; APPLICANT: Flint, Andrew J.
 ; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 ; TITLE OF INVENTION: TYROSINE PHOSPHATASES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/685,992
 ; FILING DATE: 25-JUL-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: CSHL96-03
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 781-861-6240
 ; TELEFAX: 781-861-9540
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 253 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-685-992-20

Query Match 27.4%; Score 665; DB 2; Length 253;
 Best Local Similarity 49.4%; Pred. No. 1.2e-52;
 Matches 126; Conservative 44; Mismatches 73; Indels 12; Gaps 3;
 QY 48 TVAGSRPENVKRYKDVLPDQTRVLSLQEEHSDYNGNFIKGVGPKAYVATQGP 107
 Db 4 TATGEKENVKKNRYKDILPFDHRSRVKLTLPKTPSQSDSDYINANFIKGVGPKAYVATQGP 63

QY 108 LPHTLLDFWRLVWFGVKVILMACREIENGRKRCERYW-AQEQEPQTLGFCITLILKEKW 166
 Db 64 LANTVIDFWMVWYNNVWIIVMACREFEMGRKKCERYWFLYGEDPITFAFKISC----- 118
 QY 167 LNEIDIMLRT---LKVTFOKESRVYQLQYMSWPDGRGVSSPDHMLAMVEARLQSGSP 222
 Db 119 --EDQARTDYFIRITLLLEFQNESRRLYQFHYVNNPDDHVPSSFDLSILDMISLMRYQEHED 176
 QY 223 EPLCVHCSAGCGRTGLVCTVDYVROLTLTQMIPPDFSLEFDVVLKRRQORPAAVQTEQYR 282
 Db 177 VPICIHCSAGCGRTGAICAIDYTNLLKAGKIPEEFNVNLIQEMRTORHSAVQTEQYV 236
 QY 283 FLYHTVAQMFCSLQ 297
 Db 237 LVHRAIAQLFEKQLQ 251

RESULT 10
 US-09-144-925-20
 ; Sequence 20, Application US/09144925
 ; Patent No. 5951979
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas
 ; APPLICANT: Flint, Andrew J.
 ; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 ; TITLE OF INVENTION: TYROSINE PHOSPHATASES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02421-4799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,925
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/685,992
 ; FILING DATE: July 25, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: CSHL96-032
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 781-861-6240
 ; TELEFAX: 781-861-9540
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 253 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-144-925-20

Query Match 27.4%; Score 665; DB 2; Length 253;
 Best Local Similarity 49.4%; Pred. No. 1.2e-52;
 Matches 126; Conservative 44; Mismatches 73; Indels 12; Gaps 3;
 QY 48 TVAGSRPENVKRYKDVLPDQTRVLSLQEEHSDYNGNFIKGVGPKAYVATQGP 107
 Db 4 TATGEKENVKKNRYKDILPFDHRSRVKLTLPKTPSQSDSDYINANFIKGVGPKAYVATQGP 63
 QY 108 LPHTLLDFWRLVWFGVKVILMACREIENGRKRCERYW-AQEQEPQTLGFCITLILKEKW 166

Db 64 LANTVIDFRWWEYVNVIIIVMACREPFEMGRKCCERYWPLYGDPITPAFFKISC----- 118
 Qy 167 LNEIDIMRLTAVTFOKESRSVYQLQYMSWPDGRGVPSPPDHMLAMVEBARR-----LQSG 221
 Db 119 --EDEQARTDYFILLBFQNESRRLYQFYVNNPDDHVPSPSILDMISLAKRYQEHED 176
 Qy 223 EPLCVHCSAGCGRTGVLCTVDYVYRQLLLTQMIIPDFSLFDVVLKMKRQKPAAPVQTEQYR 282
 Db 177 VPICHSAGCGRTGALCAIDYTNWLLKAGKIPEEFNVFNLIQEMTQRHSVAQTREQYE 236
 Qy 283 FLXHTVAQMFCTSLQ 297
 Db 237 LVHRAIAQLFEKQLQ 251

RESULT 11

US-08-685-992-16
 ; Sequence 16, Application US/08685992
 ; Patent No. 5912138
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas
 ; APPLICANT: Flint, Andrew J.
 ; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 ; TITLE OF INVENTION: TYROSINE PHOSPHATASES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/685,992
 ; FILING DATE: 25-JUL-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: CSHL96-03
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 781-861-6240
 ; TELEFAX: 781-861-9540
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 255 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-685-992-16

Query Match 20.4%; Score 493.5; DB 2; Length 255;
 Best Local Similarity 43.6%; Pred. No. 5.5e-37;
 Matches 115; Conservative 36; Mismatches 94; Indels 19; Gaps 7;
 Qy 47 STVAGSRPNVRKRYKDVLPYDQTRVILSLLOEGHSDYINGNFRIGVDGSLAYIATQ 106
 Db 3 SQMVASASENNAKRYRNVLPIYDWSRVLKPIHEEPCGSDYINASFMPGLWSPQEFIA 62
 Qy 107 PLPHTLLDFWRLWVEFGVKVILMACRIENGRKRCERYWAQOEPLQTLGFCITLKEKW 166
 Db 63 PLPQTVGDFWRLWVEQSSHTLVMLTNCMEAGRVCHEYWPDLDSQCTHGLRLVTLGEEV 122

Qy 167 LNEIDIMRLTAVTFOKESRSVYQLQYMSWPDGRGVPSPPDHMLAMVEBARR-----LQSG 221
 Db 123 MENVTVLLQLQVEEQK-TLSVRQFHYQAMPDHGVPSPPDILLAFWRMLRQWLQDTMEGGP 181
 Qy 222 PEPICVHCSAGCGRTGVLCTVD-YVROLLTQMTTPDFSLFDVVLKMKRQKPAAPVQTEEQ 280
 Db 182 P---IVHCSAGVGRGTLLIALDVLRLQSQEGLGP-----FSFVRKMRERPLXVQTEAQ 234
 Qy 281 YRELVHTVAQMFCTSLQNASPHYQ 304
 Db 235 YVFLH-----QCICGS-SNSQRPQ 253

RESULT 12

US-09-144-925-16
 ; Sequence 16, Application US/09144925
 ; Patent No. 5951979
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas
 ; APPLICANT: Flint, Andrew J.
 ; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 ; TITLE OF INVENTION: TYROSINE PHOSPHATASES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02421-4799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FastSeq for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,925
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/685,992
 ; FILING DATE: July 25, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: CSHL96-03Z
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 781-861-6240
 ; TELEFAX: 781-861-9540
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 255 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-144-925-16

Query Match 20.4%; Score 493.5; DB 2; Length 255;
 Best Local Similarity 43.6%; Pred. No. 5.5e-37;
 Matches 115; Conservative 36; Mismatches 94; Indels 19; Gaps 7;
 Qy 47 STVAGSRPNVRKRYKDVLPYDQTRVILSLLOEGHSDYINGNFRIGVDGSLAYIATQ 106
 Db 3 SQMVASASENNAKRYRNVLPIYDWSRVLKPIHEEPCGSDYINASFMPGLWSPQEFIA 62
 Qy 107 PLPHTLLDFWRLWVEFGVKVILMACRIENGRKRCERYWAQOEPLQTLGFCITLKEKW 166
 Db 63 PLPQTVGDFWRLWVEQSSHTLVMLTNCMEAGRVCHEYWPDLDSQCTHGLRLVTLGEEV 122
 Qy 167 LNEIDIMRLTAVTFOKESRSVYQLQYMSWPDGRGVPSPPDHMLAMVEBARR-----LQSG 221

Db 123 MENWTVLLLLQVEBQK-TLSVRQHYQAWPDHGVSPDPTLLAFWMLRQWLQDTWEGGP 181
Qy 222 PEPICVHCSAGCGRTGVLCTVD-YVRQLLLTQMIPDPDFSLFVVLKMKRKORPAAVQTEEQ 280
Db 182 P---IVHCSAGVGTGTLIALDLVLRQLQSEGLGP-----FSFVRKWRERPLVWQTEAQ 234
Qy 281 YRFLYHTVAQMFCSTLQNASPHYQ 304
Db 235 YVFLH----QCICGS-SNSQPRPQ 253
RESULT 13
US-08-342-930-2
; Sequence 2, Application US/08342930
; Patent No. 5821084
; GENERAL INFORMATION:
; APPLICANT: OLMSTED, ELIZABETH A.
; APPLICANT: MAURO, LAURA J.
; APPLICANT: DAVIS, ALAN R.
; APPLICANT: DIXON, JACK E.
; TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,930
; FILING DATE: 21-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOSKI, ANTOINETTE P.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20344-20975.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1711 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-342-930-2
Query Match 19.6%; Score 474; DB 2; Length 1711;
Best Local Similarity 39.9%; Pred. No. 5e-34;
Matches 114; Conservative 35; Mismatches 111; Indels 26; Gaps 8;
Qy 10 SELERLEARGREGAVLAGESDIQACSAWKADGVCSTVAGSRPENVRKNRYKDVLPXD 69
Db 1134 SFQSYAKSAHAHQTFQFEELKEVGKQD-----PRLEASHPNITKNRYPHVLPXD 1187
Qy 70 QTRVILSLQEGHSDYINGNFIKRGVDSGLAYIATQGLPHTLLDFWRLWEEFGVKVILM 129
Db 1188 HSRVRLTQLPGEHSDYINANFIPGYSHTQEIATQGLPKLTLEDFWRLWEEQVHVILM 1247
Qy 130 ACBEIENGRKCRERYAQOEPIQTGLFCITLKE-----KWLNEDIMRLTKVTFOKER 185
Db 1248 LTVGMENGRCEHYWPANSTPVTHGHITHLAEPEDEWTRETFQLQ--HGTEQKQ-R 1304
Qy 186 SVYQLQWSPDRGVPSPDHMLAMV-----EARRLQSGSPPELVCVHCAGCGRTGLCT 241

Db 1305 RVKQLQFTTTPDHSVPEAPSSLLAFVELVQEQVQATQCKG--PILVHCSAGVGRGT--- 1359
Qy 242 VDVYRQLLLTQMIPDP---FSLFDDVVLKMKRKORPAAVQTEEQVRFY 285
Db 1360 --FVALLRLRLQEBEKVADVNTVYILRLHRLPLMIQTLTSQYIFLH 1403
RESULT 14
US-08-202-389-6
; Sequence 6, Application US/08202389
; Patent No. 5536636
; GENERAL INFORMATION:
; APPLICANT: Freeman Jr., Robert M.
; APPLICANT: Plutsky, Jorge
; APPLICANT: Neel, Benjamin G.
; APPLICANT: Rosenberg, Robert D.
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE
; TITLE OF INVENTION: PHOSPHATASES HAVING SH2 DOMAINS
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,389
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,926
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,141
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/721,112
; FILING DATE: 26-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BIH92-05WA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-202-389-6
Query Match 19.3%; Score 467; DB 1; Length 595;
Best Local Similarity 32.5%; Pred. No. 4.8e-34;
Matches 112; Conservative 57; Mismatches 109; Indels 62; Gaps 10;
Qy 22 EGAVLAG---BFSDIQACSAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSL 78
Db 237 EDTACAGWFESFIQ-----KQEVKNLHQRLEGQRPENKGNRYKNLLPPDHSVIL--- 289
Qy 79 QEEGH-----SDYINGNFIKRV-----DGLAYIATQGLPHTLLDFWRLWEEFGVKVI 127
Db 290 --QGSDNSIPGSDYINANYIKNQLLGPDENAKTYIASQGCLEATVDFWQMAWQENSRI 347
Qy 128 LMACEIEINGKRCERYWAQOEPLQTLGFCITILKEKWLNEDIMRLTKVTFOKES--- 184

Db 348 VMTTREVKEGKNCVYPWPEVGMQRAYGPYSVTNVGEHDTTE-YKLRITLQVSLDNGDLI 406
 Qy 185 RSVYQLQYMWPDGVPSSPDHMLAMVEBARLQSGPE--PLCVHCSAGCGRTGVLCTV 242
 Db 407 REIWHYQYLSWPDHGVSEPGVLSFLDQINQRESLPHAGPIIIVHCSAGIGRTGTIIVI 466
 Qy 243 DYVRQLLLTQMIIPDPFSLFDVWLKMRKORPAAVQTEQYRFLYHTVAQMFCSF----- 395
 Db 467 DMLMENISTKGLDCDDIDIQTIQWRAQRSGMVQTEAQYKFIYVAIAQFIETTKKLEVL 526
 Qy 296 -----LQNA-----SPHYQNIKEN 309
 Db 527 QSQKGSEYGNITYPPAMKNNAHAKASRTSSKHEDVYEN 566

 RESULT 15
 US-08-202-389-8
 ; Sequence 8, Application US/08202389
 ; Patent No. 5536636
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman Jr., Robert M.
 ; APPLICANT: Plutsky, Jorge
 ; APPLICANT: Neel, Benjamin G.
 ; APPLICANT: Rosenberg, Robert D.
 ; TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE
 ; NUMBER OF INVENTION: PHOSPHATASES HAVING SH2 DOMAINS
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/202,389
 ; FILING DATE: 28-FEB-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/983,926
 ; FILING DATE: 01-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/829,141
 ; FILING DATE: 31-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/721,112
 ; FILING DATE: 26-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: BIH92-05VA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 861-6240
 ; TELEFAX: (617) 861-9540
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 631 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-202-389-8

Query Match 19.2%; Score 465; DB 1; Length 631;
 Best Local Similarity 30.9%; Pred. No. 8e-34;
 Matches 126; Conservative 62; Mismatches 136; Indels 84; Gaps 14;

Db 237 EDTAKAGFWEEFESLQ----KQEVKNLHQLEQORPENKGNRYKNILPPDHSRVIL--- 289
 Qy 79 QEEGH-----SDYINGNFIRGV-----DGLAVIATQGPLPHTLLDFWRLVWVEFGVKVI 127
 Db 290 --QGRDNI PGSDYINANYIKNQLLGPDENAKTVIASGGCLEATVNDFWQMAQENSRVI 347
 Qy 128 LMACREIENGKRCERYWAQEQEPLQTGLFCITLTIKEKWLNEIMLTLLKVTQKES--- 184
 Db 348 VMTTREVKEGKNCVYPWPEVGMQRAYGPYSVTNVGEHDTTE-YKLRITLQVSLDNGDLI 406
 Qy 185 RSVYQLQYMWPDGVPSSPDHMLAMVEBARLQSGPE--PLCVHCSAGCGRTGVLCTV 242
 Db 407 REIWHYQYLSWPDHGVSEPGVLSFLDQINQRESLPHAGPIIIVHCSAGIGRTGTIIVI 466
 Qy 243 DYVRQLLLTQMIIPDPFSLFDVWLKMRKORPAAVQTEQYRFLYHTVAQMFCSF----- 295
 Db 467 DMLMENISTKGLDCDDIDIQTIQWRAQRSGMVQTEAQYKFIYVAIAQFIETTKKLEVL 526
 Qy 296 -----LQNA-----SPHYQNIKENCAPLY-----DDALFLR 321
 Db 527 QSQKGSEYGNITYPPAMKNNAHAKASRTSSKHEDVYEN---LHTKNKEESEEAASVR 583
 Qy 322 T-----PQALLAIPRPPGGVLRISISVPGSPGHAMADTYAEQKRGAP 363
 Db 584 QGEEQGFQPEVS-----GAVLRWPCLSPPDVEAFRDGQTHNLNLGYP 626

Search completed: August 17, 2004, 20:45:05
 Job time : 20 secs

Qy 22 EGAVLAG---EFSDIQACSAANKADGVCSIVAGSRPNVKNYKDVLPYDQTRVILSL 78

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:44:11 ; Search time 47 Seconds

(without alignments)
3059.120 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 2424

Sequence: 1 MSRLDSARSFLERLEARGG.....NLRIGPKGRDPPAEWTRV 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2424	100.0	458	13	US-10-087-993-36
2	1754.5	72.4	453	14	Sequence 36, Appl
3	1724.5	71.1	448	13	Sequence 7, Appl
4	755.5	31.2	802	9	Sequence 32, Appl
5	755.5	31.2	802	15	Sequence 18, Appl
6	755.5	31.2	802	15	Sequence 95, Appl
7	727.5	30.0	807	9	Sequence 5, Appl
8	709	29.2	780	15	Sequence 2, Appl
9	709	29.2	780	15	Sequence 69, Appl
10	708	29.2	692	15	Sequence 71, Appl
11	708	29.2	778	16	Sequence 4, Appl
12	708	29.2	808	15	Sequence 848, App
13	706	29.1	773	16	Sequence 2, Appl
14	705.5	29.1	382	15	Sequence 845, App
15	703	29.0	775	15	Sequence 77, Appl
					Sequence 75, Appl

Sequence 21, Appl
Sequence 94, Appl
Sequence 94, Appl
Sequence 819, App
Sequence 93, Appl
Sequence 93, Appl
Sequence 6, Appl
Sequence 17, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 8, Appl
Sequence 97, Appl
Sequence 23, Appl
Sequence 1, Appl
Sequence 87, Appl
Sequence 91, Appl
Sequence 85, Appl
Sequence 3086, Ap
Sequence 117, App
Sequence 119, App
Sequence 2, Appl
Sequence 26, Appl
Sequence 2, Appl
Sequence 14, Appl
Sequence 13, Appl
Sequence 3, Appl
Sequence 28, Appl
Sequence 30, Appl
Sequence 32, Appl
Sequence 789, App

665 27.4 312 9 US-09-788-626-21
523 21.6 235 12 US-10-087-684-94
523 21.6 235 12 US-10-218-779-94
523 21.6 235 12 US-10-072-012-819
521.5 21.5 263 12 US-10-087-684-93
521.5 21.5 263 12 US-10-218-779-93
496.5 20.5 264 14 US-10-245-539-6
493.5 20.4 313 9 US-09-788-626-17
491.5 20.3 1093 14 US-10-245-539-4
491.5 20.3 1118 14 US-10-245-539-2
491.5 20.3 1118 14 US-10-245-539-8
482.5 19.9 613 15 US-10-366-547-97
463.5 19.1 341 9 US-09-788-626-23
463 19.1 595 9 US-09-920-021A-1
463 19.1 595 15 US-10-366-547-87
463 19.1 595 15 US-10-366-547-91
463 19.1 597 15 US-10-366-547-89
463 19.1 621 15 US-10-264-049-3086
463 19.1 843 14 US-10-072-036-117
463 19.1 853 14 US-10-072-036-119
458 18.9 593 14 US-10-262-552-2
458 18.9 593 14 US-10-366-547-26
458 18.9 593 16 US-10-703-210-2
456 18.8 322 9 US-09-788-626-14
454 18.7 325 9 US-09-788-626-13
453 18.7 593 9 US-09-920-021A-3
453 18.7 593 15 US-10-366-547-28
453 18.7 593 15 US-10-366-547-30
453 18.7 593 15 US-10-366-547-32
453 18.7 593 15 US-10-444-795B-789

ALIGNMENTS

RESULT 1
US-10-087-993-36
; Sequence 36, Application US/10087993
; Publication No. US20020169303A1
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; Aoki, Naohito
; Kim, Yeong Woong
; Wang, Hong Yang
; Chen, Zhengjun
; Naylor, Oliver
; Kharitonov, Alexei Igorevich
; TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDPI, CLK
; AND SIRP POLYPEPTIDES AND RELATED
; PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/087,993
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,150
; FILING DATE: June 17, 1997
; APPLICATION NUMBER: U.S. 60/019,629

; FILING DATE: June 17, 1996
 ; APPLICATION NUMBER: U.S. 60/023,485
 ; FILING DATE: August 9, 1996
 ; APPLICATION NUMBER: U.S. 60/030,860
 ; FILING DATE: No. US20020169303A1ember 13, 1996
 ; APPLICATION NUMBER: U.S. 60/034,286
 ; FILING DATE: December 19, 1996
 ; APPLICATION NUMBER: U.S. 60/030,964
 ; FILING DATE: No. US20020169303A1ember 15, 1996
 ;
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 225/298
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ;
 ; INFORMATION FOR SEQ ID NO: 36:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 458 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
 US-10-087-993-36

Query Match 100.0%; Score 2424; DB 13; Length 458;
 Best Local Similarity 100.0%; Pred. No. 1.8e-199;
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSRLDSARGFLELRARGREGAVLAGFSDIOACSAAWKADGVCSVAGSPENVRKN 60
 DB 1 MSRLDSARGFLELRARGREGAVLAGFSDIOACSAAWKADGVCSVAGSPENVRKN 60
 QY 61 RYKDVLPYDQTRVLSLQEEGSHDYINGNFIKRGVDSLAYIATQGPLHTLDFWRLV 120
 DB 61 RYKDVLPYDQTRVLSLQEEGSHDYINGNFIKRGVDSLAYIATQGPLHTLDFWRLV 120
 QY 121 EFGVKVILMACREIENGKRCERYWAQEQPLQGLFCITLKEKWLNEIMLRTLKVT 180
 DB 121 EFGVKVILMACREIENGKRCERYWAQEQPLQGLFCITLKEKWLNEIMLRTLKVT 180
 QY 181 QKESRSVYQLOYSWPDGRGVSPDPHMLAMVEARLQGSPEPLCVHCSAGCGRTGVL 240
 DB 181 QKESRSVYQLOYSWPDGRGVSPDPHMLAMVEARLQGSPEPLCVHCSAGCGRTGVL 240
 QY 241 TVDYVROLLLTQMTPPDFSLFDVVLKMKRKPAAVQTEEQRYFLYHTVAQMFCS 300
 DB 241 TVDYVROLLLTQMTPPDFSLFDVVLKMKRKPAAVQTEEQRYFLYHTVAQMFCS 300
 QY 301 PHYQNIKENCAPLYDDALFLRTPOALLAI PRPPGGVLRISVPGSPGHAMADTYAE 360
 DB 301 PHYQNIKENCAPLYDDALFLRTPOALLAI PRPPGGVLRISVPGSPGHAMADTYAE 360
 QY 361 GAPAGAGSGTGTGTGARGAABEAPLYSKVTPRAQRGAHAEDARGTLPGRVAD 420
 DB 361 GAPAGAGSGTGTGTGARGAABEAPLYSKVTPRAQRGAHAEDARGTLPGRVAD 420
 QY 421 SGAYEDVAGGAQTGGLGNLRIGRPGKPRDPPAEWTRV 458
 DB 421 SGAYEDVAGGAQTGGLGNLRIGRPGKPRDPPAEWTRV 458

RESULT 2

US-10-243-687-7
 ; Sequence 7, Application US/10243687
 ; Publication No. US20030073120A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aoki, Naohito
 ; Ullrich, Axel
 ; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
 ; AND RELATED PRODUCTS AND METHODS

; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; Suite 4700
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Fast-SEQ for Windows 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/243,687
 ; FILING DATE: 16-Sep-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/430,626A
 ; FILING DATE: 29-Oct-1999
 ; APPLICATION NUMBER: 08/951,260
 ; FILING DATE: October 16, 1997
 ; APPLICATION NUMBER: 60/030,860
 ; FILING DATE: No. US20030073120A1ember 13, 1996
 ; APPLICATION NUMBER: PCT/1897/00946
 ; FILING DATE: June 17, 1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 227/004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 453 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-10-243-687-7

Query Match 72.4%; Score 1754.5; DB 14; Length 453;
 Best Local Similarity 74.5%; Pred. No. 5.9e-142;
 Matches 342; Conservative 37; Mismatches 73; Indels 7; Gaps 3;
 QY 1 MSRLDSARGFLELRARGREGAVLAGFSDIOACSAAWKADGVCSVAGSPENVRKN 60
 DB 1 MSRLDSARGFLELRARGREGAVLAGFSDIOACSAAWKADGVCSVAGSPENVRKN 60
 QY 61 RYKDVLPYDQTRVLSLQEEGSHDYINGNFIKRGVDSLAYIATQGPLHTLDFWRLV 120
 DB 61 RYKDVLPYDQTRVLSLQEEGSHDYINGNFIKRGVDSLAYIATQGPLHTLDFWRLV 120
 QY 121 EFGVKVILMACREIENGKRCERYWAQEQPLQGLFCITLKEKWLNEIMLRTLKVT 180
 DB 121 EFGVKVILMACREIENGKRCERYWAQEQPLQGLFCITLKEKWLNEIMLRTLKVT 180
 QY 181 QKESRSVYQLOYSWPDGRGVSPDPHMLAMVEARLQGSPEPLCVHCSAGCGRTGVL 240
 DB 181 QKESRSVYQLOYSWPDGRGVSPDPHMLAMVEARLQGSPEPLCVHCSAGCGRTGVL 240
 QY 241 TVDYVROLLLTQMTPPDFSLFDVVLKMKRKPAAVQTEEQRYFLYHTVAQMFCS 300
 DB 241 TVDYVROLLLTQMTPPDFSLFDVVLKMKRKPAAVQTEEQRYFLYHTVAQMFCS 300
 QY 301 PHYQNIKENCAPLYDDALFLRTPOALLAI PRPPGGVLRISVPGSPGHAMADTYAE 360
 DB 301 PHYQNIKENCAPLYDDALFLRTPOALLAI PRPPGGVLRISVPGSPGHAMADTYAE 360

QY 361 GAPAGAGSGTGTGTGARGAEEAPLYSKVTPRAQPGAHAEADARGTLP-GRVPADQSPA 419
Db 361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTEAQAQGTALGRVPADENPS 414
QY 420 GSGAYSDVAGAGTGGGLGFLNLRIGRPKGRDPPAEWTRV 458
Db 415 GPDAYEEVTDGAQTGGGLGFLNLRIGRPKGRDPPAEWTRV 453

RESULT 3

US-10-087-993-32
; Sequence 32, Application US/10087993
; Publication No. US20020169303A1
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; Aoki, Naohito
; Kim, Yeong Woong
; Wang, Hong Yang
; Chen, Zhengjun
; Naylor, Oliver
; Kharitonov, Alexei Igorevich
; TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,
; AND SIRP POLYPEPTIDES AND RELATED
; PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/087.993
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,150
; FILING DATE: June 17, 1997
; APPLICATION NUMBER: U.S. 60/019,629
; FILING DATE: June 17, 1996
; APPLICATION NUMBER: U.S. 60/023,485
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: U.S. 60/030,860
; FILING DATE: No. US20020169303A1ember 13, 1996
; APPLICATION NUMBER: U.S. 60/034,286
; FILING DATE: December 19, 1996
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: No. US20020169303A1ember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-10-087-993-32

Query Match 71.1%; Score 1724.5; DB 13; Length 448;
Best Local Similarity 74.2%; Pred. No. 2.2e-139;
Matches 337; Conservative 37; Mismatches 73; Indels 7; Gaps 3;
QY 1 MSRSLSARSFLERLEARGGREGAVLAGEPFSDIQACSAAMKADGVCSTVAGSRPENVRKN 60
Db 1 MSRQSDLVRSFLEQQEARDHRKGAILAREFSDIKARSVAMKTEGVCSTKAGSQQNSKKN 60
QY 61 RYKDVLPYDQTRVLSLLQEEGHSYINGNFIIRGVDGSLAYIATOGPLPHTLLDFWRLVW 120
Db 61 RYKDVVPYDETFVLSLLQEEGHGDIYINANFIRGTDGSCAYIATOGPLPHTLLDFWRLVW 120
QY 121 EFGVKVILMACREIENGKRRCERYWAQOEPLQTGLFCITILKEKWLNEDIMRLTKWTF 180
Db 121 EFGIKVILMACQETENGRRKRCERYWAQEREPLQAGPFCCITLTKETALTSDITLRTQVTF 180
QY 181 OKESRSVYQLOVMSWPDGRGVSSPDHMLAMVEEARLQSGSPEPLCVHCSAGCGRTGVLC 240
Db 181 QKESRPVHLQVMSWPDHGVFSSSDHILTWEEARCLQGLGFGPLCVHCSAGCGRTGVLC 240
QY 241 TVDYVRQLLLTQMIPPDFSLFDVVLKMKRQKPAAVQTEEQYRFLYHTVAQMFCSLTQNAS 300
Db 241 AVDYVRQLLLTQTIPPNPSLFEVLEMRKQPAAVQTEEQYRFLYHTVAQLFSTRLOQNS 300
QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAI P3PPGGVLESISVPGSPGHAMADTVAEEOKR 360
Db 301 PLYQNLKENRAPICKDSSSLRTSSALPATSRPLGVLRSISVPGPPTLPDMADTVAVQKR 360
QY 361 GAPAGAGSGTGTGTGARGAEEAPLYSKVTPRAQPGAHAEADARGTLP-GRVPADQSPA 419
Db 361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTEAQAQGTALGRVPADENPS 414
QY 420 GSGAYSDVAGAGTGGGLGFLNLRIGRPKGRDPPA 453
Db 415 GPDAYEEVTDGAQTGGGLGFLNLRIGRPKGRDPPA 448

RESULT 4

US-09-822-295-18
; Sequence 18, Application US/09822295
; Patent No. US20020119501A1
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; Gregory D. Plowman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; PTPO4 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/822,295
; FILING DATE: 02-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/081,345
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 234/253
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-822-295-18

Query Match 31.2%; Score 755.5; DB 9; Length 802;
Best Local Similarity 44.0%; Pred. No. 9.2e-56;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;
QY 27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLOEGHSDY 86
DB 25 ASEFLKLRQSTKYKADKIYPTTVAQRPNKIKKNRYKDILPYDHSLSVELSLTSDSSY 84
QY 87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWELVWFGVKVILMACRIENGRKRCERYA 146
DB 85 INASFIKGVGPKAYIATQGPLSTLLDFWRMIWEYRILVIVMACMEFEMGKKCCERYA 144
QY 147 QEQE-PLQTGLFCITLKEKWLNEDIMRLTKVTFQKESRSVYQLOYSWMPDRGVPSSPD 205
DB 145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNETRIIYQHYKNWPDHVPSSID 203
QY 206 HMLAMVEARLQSGGPEPLCHCSAGCGRTGVLCTVDYVRQLLLTQMIPDFSLFDVVL 265
DB 204 PIQLIWMRCYQEDDCVPCICHSAGCGRTGVCADVDYTWMLLKDGIIIPKNSFVFNLIQ 263
QY 266 KMRKORPAAVOTEQRYFLYHTVAQMFCSLTQNASPHYQNIKENCAPLYDDALFLRTPQA 325
DB 264 EMRTQPSLVQTQOYELVSAVLELF-----KRMVDVISDNHLG-----REIQA 308
QY 326 LLATPRPPGGVLRISVPGS-----PGHADV--TYAEQKRGAPAGAGSGTGTGTG 377
DB 309 QCSIFE-----QSLTVEADSCPLDLPKNAMRDVKTTHQHSKQGAEAESTGGSLGLRTS 362
QY 378 ARSAEE 383
DB 363 TMAEE 368

RESULT 5
US-10-366-547-95
Sequence 95, Application US/10366547
Publication No. US20030215899A1
GENERAL INFORMATION:
APPLICANT: Meng, Tzu-Ching
APPLICANT: Tonks, Nicholas K.
APPLICANT: Cool, Deborah E.
TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
FILE REFERENCE: 200125.439
CURRENT APPLICATION NUMBER: US/10/366,547
CURRENT FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 95
LENGTH: 802
TYPE: PRP
ORGANISM: Mus musculus
US-10-366-547-95

Query Match 31.2%; Score 755.5; DB 15; Length 802;
Best Local Similarity 44.0%; Pred. No. 9.2e-56;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;

QY 27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLOEGHSDY 86
DB 25 ASEFLKLRQSTKYKADKIYPTTVAQRPNKIKKNRYKDILPYDHSLSVELSLTSDSSY 84
QY 87 INGNFIRGVDGSLAYIATQGPLPHTLLDFWELVWFGVKVILMACRIENGRKRCERYA 146
DB 85 INASFIKGVGPKAYIATQGPLSTLLDFWRMIWEYRILVIVMACMEFEMGKKCCERYA 144
QY 147 QEQE-PLQTGLFCITLKEKWLNEDIMRLTKVTFQKESRSVYQLOYSWMPDRGVPSSPD 205
DB 145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNETRIIYQHYKNWPDHVPSSID 203
QY 206 HMLAMVEARLQSGGPEPLCHCSAGCGRTGVLCTVDYVRQLLLTQMIPDFSLFDVVL 265
DB 204 PIQLIWMRCYQEDDCVPCICHSAGCGRTGVCADVDYTWMLLKDGIIIPKNSFVFNLIQ 263
QY 266 KMRKORPAAVOTEQRYFLYHTVAQMFCSLTQNASPHYQNIKENCAPLYDDALFLRTPQA 325
DB 264 EMRTQPSLVQTQOYELVSAVLELF-----KRMVDVISDNHLG-----REIQA 308
QY 326 LLATPRPPGGVLRISVPGS-----PGHADV--TYAEQKRGAPAGAGSGTGTGTG 377
DB 309 QCSIFE-----QSLTVEADSCPLDLPKNAMRDVKTTHQHSKQGAEAESTGGSLGLRTS 362
QY 378 ARSAEE 383
DB 363 TMAEE 368

RESULT 6
US-10-309-423-5
Sequence 5, Application US/10309423
Publication No. US20040006777A1
GENERAL INFORMATION:
APPLICANT: HSC Research and Development Limited Partnership
TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases
FILE REFERENCE: 92906-2
CURRENT APPLICATION NUMBER: US/10/309,423
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/600,358
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: CA 2,220,853
PRIOR FILING DATE: 1998-01-16
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 802
TYPE: PRP
ORGANISM: Mus musculus
US-10-309-423-5

Query Match 31.2%; Score 755.5; DB 15; Length 802;
Best Local Similarity 44.0%; Pred. No. 9.2e-56;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;

Db 264 EMRTORSLSVQTQEOYELVYSAVLELF-----KRHMVDISDNLHG-----REIQ A 308
Qy 326 LLAI PRPGVGLRSISVPGS-----PGHAMAD--TYAEQKRGAPAGAGSGTQTGTG 377
Db 309 QCSIP E-----OSLTVEADSCPLDLPKNMRDVKTTNQHSGKQGAESGTGSSGLRTS 362
Qy 378 ARSAEE 383
Db 363 TMAEE 368
RESULT 7
US-09-822-295-2
; Sequence 2, Application US/09822295
; Patent No. US20020119501A1
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; Gregory D. Plowman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; PTP04 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM: Diskette, 1.44 Mb
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/822,295
; FILING DATE: 02-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/081,345
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/253
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-822-295-2
Query Match 30.0%; Score 727.5; DB 9; Length 807;
Best Local Similarity 46.9%; Pred. No. 2.4e-53;
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;
Qy 27 AGEFSIDIOACSAANKADGVCSTVAGSRPNVRKRYKDVLPYDQTRVILSLQEEGHSY 86
Db 25 ANEFLKLRQSTKYKADKTYPTTVAEKPKNIKKNRYKDILPYDYSRVLSLITSDSSY 84
Qy 87 INGNFIRGVDGLAYIATQGPLHTLLDFWLVWFEGVKVILMACREIENGRKRCERYWA 146
Db 85 INANFIKGVGPKYAIATQGPLSTLLDFWLVWFEGVKVILMACREIENGRKRCERYWA 144
Qy 147 QEQLPQTGLFCITLIKELKWLNEDIMLRTLKVTFOKESRSVYQLQYMSWPDRCVPSPPD 205

Db 145 EPGENQLSFGPFSVSCAEAK-RKSDYIIRTILKXFNSETRIIYQFHYKNWEDHVPSSID 203
Qy 206 HMLAWVEARLRQSGPPLCVHCSAGCGRTGVLCTVYVQQLLTQMIPTDFSLFDVVL 265
Db 204 PILELIWDVRCYQEDSDSVPICHCSAGCGRTGVICAIDYTWMLKDGIPENFSVSLIR 263
Qy 266 KMRKORPAAVOTEEOYRFLYHTVAMF---CSTLQNASPHYCNIKENCAP 312
Db 264 EMRTORSLSVQTQEOYELVYSAVLELF-----KRHMVDISDNLHG-----REIQ A 308
RESULT 8
US-10-366-547-69
; Sequence 69, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
; APPLICANT: Meng, Tzu-Ching
; APPLICANT: Tonks, Nicholas K.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
; FILE OF INVENTION: PHOSPHATASES
; FILE REFERENCE: 200125.439
; CURRENT APPLICATION NUMBER: US/10/366,547
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-547-69
Query Match 29.2%; Score 709; DB 15; Length 780;
Best Local Similarity 41.0%; Pred. No. 8.8e-52;
Matches 144; Conservative 65; Mismatches 116; Indels 26; Gaps 7;
Qy 9 RSFLERLEA-----RGREGAVLAGEFSDIOACSAANKADGVCSTVAGSRPNVRKRYK 63
Db 8 RKFIOGVQAMKSPDHNGEDN--FARDFMLRLRLSTKYTEKIYPTATGEENVAKNRYK 65
Qy 64 DVLVYDQTRVILSLQEEGHSYINGNFIIRGVDGLAYIATQGPLHTLLDFWLVWFEG 123
Db 66 DILPFDHRSVKULTKTPQSDSDYINANIKGVYGPKAIVATQGPLANTVIDFWRMVWYN 125
Qy 124 VKVILMACREIENGRKRCERYW-AQEQLPQTGLFCITLIKELKWLNEDIMLRTLKVTFOK 182
Db 126 VVILVMAKREFEMGRKRCERYWPLYGEDPITPAPFKIS-CEDEQARTDYFIRTLLEFQN 184
Qy 183 ERSRVYQLQYMSWPDRCVPSPDHMLAMVEARLRQSGPPLCVHCSAGCGRTGVLCTV 242
Db 185 ESRRLYQHYVNPDPHDVPSDFSILDMISLMRKYQEHEDVPICHCAGCGRTGAICAI 244
Qy 243 DYVRQLLTQMIPTDFSLFDVVLKMRKORPAAVOTEEOYRFLYHTVAMFSTLQNASPH 302
Db 245 DYTWNLLKAGKIPESFNFNLIQEVRTQHSVAVQTKQYELVHRAIAQLFEKQLQLYEIH 304
Qy 303 YONIKENCAPLYDDALFLRTPOALLAI-----PRPGVGLRSISVPG 344
Db 305 -----GAQKIADGVNEINTENNVSSIEPFEKQDSPPKPPR--TRSCILVEG 347
RESULT 9
US-10-366-547-71
; Sequence 71, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
; APPLICANT: Meng, Tzu-Ching
; APPLICANT: Tonks, Nicholas K.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
; FILE OF INVENTION: PHOSPHATASES
; FILE REFERENCE: 200125.439


```

; PRIOR APPLICATION NUMBER: CA 2,220,853
; PRIOR FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 808
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-423-2

Query Match      29.2%; Score 708; DB 15; Length 808;
Best Local Similarity 46.7%; Pred. No. 1.1e-51;
Matches 136; Conservative 54; Mismatches 95; Indels 6; Gaps 4;

Qy 27 AGFSDIOAASAAWADGVSTVAGSPENVRKNRYKDVLPYQTRVILSLQEGHSDY 86
Dy 25 ANEFLKROSTKYADKTYPTTVAENAKNKKRYKXILPYDYSRVELSLITSDSSY 84
Qy 87 INGNFIRGVGSLAYIATQGPLHTLLDFWELWVEFGVKVILMACREIENGRKCRERYA 146
Dy 85 INANFIRGVGPKAYIATQGPLSTLLDFWELWVEFVSVLIVMACMEYENGRKCRERYA 144
Qy 147 QEQF-PLQTGLFCITLKEKWLNEIMRLTKVTFQKESRVYQLOQYMSWPDGRVSPSD 205
Dy 145 EPGEMQLFPGFVSCEAEK-RKSDYIIRTLKVKFNSETRTIYQHYKNWFDHVPSSID 203
Qy 206 HMLAWBEARLQSGPEPLCVHCSAGCGRTGVLCT-VDYVQRLITQMTPPDPSLDVY 254
Dy 204 PILELIWDVRCYQEDDSVPCIHCSAGCGRTGVCALVDYTMLLKDGIIIPENFVSFLI 263
Qy 265 LKMKRQRPAAVQTEQRYFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
Dy 264 REMATQRPVLVQTEQRYELVYNAVLFLFKQMDVIRDKHSGTSQAKHCIP 314

RESULT 13
US-10-322-281-845
; Sequence 845, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 845
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-322-281-845

Query Match      29.1%; Score 706; DB 16; Length 773;
Best Local Similarity 25.5%; Pred. No. 1.6e-51;
Matches 196; Conservative 86; Mismatches 163; Indels 324; Gaps 20;

Qy 9 RSFLERLEA-----RGGREGAVLAGEFSDIOACSAAMKADGVCTVAGSPENVRKNRYK 63
Dy 8 RRFQIRVQAMKSPDHNGEDN--FARDFMRLRLSTKYRTEKIYPTATGEKEENVKKNRYK 65
Qy 64 DVLVYDQTRVILSLQEGHSDYINGNFIQVDSGLAYIATQGPLHTLLDFWELWVEFG 123
Dy 66 DILPFDHRSVKLTLTQPSQSDYINANFIKGVYGPAYVATQGPLANTVIDFWRMTWEYN 125
Qy 124 VKVILMACREIENGRKCRERYA-AQEQPLQTLGFCITLKEKWLNEIMRLTKVTFQK 182
Dy 126 VVILVACRFEMGRKKCRERYWPLYGDDPTTFAPFKISCENEO-ARTDYFIRTLLEFQN 184
Qy 183 ESRVYQLOQMSWPDGRVSPSDHMLAWBEARLQSGPEPLCVHCSAGCGRTGVLCTV 242
Dy 185 ESRLYQHYVNWEDHVPSSFDILDWISLMRYQEHEDVDPICIHCSAGCGRTGALCAI 244

; PRIOR APPLICATION NUMBER: CA 2,220,853
; PRIOR FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 808
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-423-2

Query Match      29.2%; Score 708; DB 15; Length 808;
Best Local Similarity 46.7%; Pred. No. 1.1e-51;
Matches 136; Conservative 54; Mismatches 95; Indels 6; Gaps 4;

Qy 27 AGFSDIOAASAAWADGVSTVAGSPENVRKNRYKDVLPYQTRVILSLQEGHSDY 86
Dy 25 ANEFLKROSTKYADKTYPTTVAENAKNKKRYKXILPYDYSRVELSLITSDSSY 84
Qy 87 INGNFIRGVGSLAYIATQGPLHTLLDFWELWVEFGVKVILMACREIENGRKCRERYA 146
Dy 85 INANFIRGVGPKAYIATQGPLSTLLDFWELWVEFVSVLIVMACMEYENGRKCRERYA 144
Qy 147 QEQF-PLQTGLFCITLKEKWLNEIMRLTKVTFQKESRVYQLOQYMSWPDGRVSPSD 205
Dy 145 EPGEMQLFPGFVSCEAEK-RKSDYIIRTLKVKFNSETRTIYQHYKNWFDHVPSSID 203
Qy 206 HMLAWBEARLQSGPEPLCVHCSAGCGRTGVLCT-VDYVQRLITQMTPPDPSLDVY 254
Dy 204 PILELIWDVRCYQEDDSVPCIHCSAGCGRTGVCALVDYTMLLKDGIIIPENFVSFLI 263
Qy 265 LKMKRQRPAAVQTEQRYFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
Dy 264 REMATQRPVLVQTEQRYELVYNAVLFLFKQMDVIRDKHSGTSQAKHCIP 314

RESULT 13
US-10-322-281-845
; Sequence 845, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 865
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 845
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-322-281-845

Query Match      29.1%; Score 706; DB 16; Length 773;
Best Local Similarity 25.5%; Pred. No. 1.6e-51;
Matches 196; Conservative 86; Mismatches 163; Indels 324; Gaps 20;

Qy 9 RSFLERLEA-----RGGREGAVLAGEFSDIOACSAAMKADGVCTVAGSPENVRKNRYK 63
Dy 8 RRFQIRVQAMKSPDHNGEDN--FARDFMRLRLSTKYRTEKIYPTATGEKEENVKKNRYK 65
Qy 64 DVLVYDQTRVILSLQEGHSDYINGNFIQVDSGLAYIATQGPLHTLLDFWELWVEFG 123
Dy 66 DILPFDHRSVKLTLTQPSQSDYINANFIKGVYGPAYVATQGPLANTVIDFWRMTWEYN 125
Qy 124 VKVILMACREIENGRKCRERYA-AQEQPLQTLGFCITLKEKWLNEIMRLTKVTFQK 182
Dy 126 VVILVACRFEMGRKKCRERYWPLYGDDPTTFAPFKISCENEO-ARTDYFIRTLLEFQN 184
Qy 183 ESRVYQLOQMSWPDGRVSPSDHMLAWBEARLQSGPEPLCVHCSAGCGRTGVLCTV 242
Dy 185 ESRLYQHYVNWEDHVPSSFDILDWISLMRYQEHEDVDPICIHCSAGCGRTGALCAI 244

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US-10-366-547-77
; Sequence 77, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
; APPLICANT: Meng, Tzu-Ching
; APPLICANT: Tonks, Nicholas K.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASES
; FILE REFERENCE: 200125.439
; CURRENT APPLICATION NUMBER: US/10/366,547
; CURRENT FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-366-547-77

```

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Query Match      29.1%; Score 705.5; DB 15; Length 382;
Best Local Similarity 45.1%; Pred. No. 6.5e-52;
Matches 133; Conservative 59; Mismatches 94; Indels 9; Gaps 4;

Qy 9 RSFLERLEA-----RGGREGAVLAGEFSDIOACSAAMKADGVCTVAGSPENVRKNRYK 63
Dy 8 RRFQIRVQAMKSPDHNGEDN--FARDFMRLRLSTKYRTEKIYPTATGEKEENVKKNRYK 65
Qy 64 DVLVYDQTRVILSLQEGHSDYINGNFIQVDSGLAYIATQGPLHTLLDFWELWVEFG 123
Dy 66 DILPFDHRSVKLTLTQPSQSDYINANFIKGVYGPAYVATQGPLANTVIDFWRMTWEYN 125
Qy 124 VKVILMACREIENGRKCRERYA-AQEQPLQTLGFCITLKEKWLNEIMRLTKVTFQK 182

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Db 126 VVIIVMACREFEMGRKCRWPLYGDPITFAPFKISCENEQ-ARTDYFIRTLLEFQN 184
 Qy 183 ESRVYQLQYMSWDRGVSPDRLMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVLCTV 242
 Db 185 ESRLYQHYVNWPDHVPSSFDSDILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244
 Qy 243 DYVRQLLLTQMIPPDFSLFDVVLKMRKORPAAVQTEQYRFLYHTVAQMFCSLTQ 297
 Db 245 DYTWNLLKAGKIPPEFNVFNLIQEMRTQRHSVQTKQYELVHRAIAQLFEKQLQ 299

RESULT 15
 US-10-366-547-75
 ; Sequence 75, Application US/10366547
 ; Publication No. US20030215899A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meng, Tzu-Ching
 ; APPLICANT: Tonks, Nicholas K.
 ; APPLICANT: Cool, Deborah E.
 ; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
 ; TITLE OF INVENTION: PHOSPHATASES
 ; FILE REFERENCE: 200125, 439
 ; CURRENT APPLICATION NUMBER: US/10/366,547
 ; CURRENT FILING DATE: 2003-02-12
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 75
 ; LENGTH: 775
 ; TYPE: PRT
 ; ORGANISM: Mus. musculus
 US-10-366-547-75

Query Match 29.0%; Score 703; DB 15; Length 775;
 Best Local Similarity 25.0%; Pred. No. 2.9e-51;
 Matches 194; Conservative 84; Mismatches 162; Indels 336; Gaps 17;

Qy 9 RSFLERLEA-----RGREGAVLAGESDSDIQASAAWKADGVCSVTAGSPENVRKNRYK 63
 Db 8 RRFQVQAMKSPDHNGEDN--FARDFMRLRLRSTKRYTEKIYPTATGEBENVRKNRYK 65

Qy 64 DVLFPDQTRVILSLQEGHSDYINGFIRGVDGSLAYIATQGPLHTLDFWRLVWFEFG 123
 Db 66 DILFDSHRVKLTLSQSDSDYINAFIKGVYGPXAVYATQGFRTVIDFWRMWYFN 125

Qy 124 VKVILMACREIENGRKCRWY-AQOEPLQTLFCITLKEKWLNEIDIMRLTKYTFQK 182
 Db 126 VVIIVMACREFEMGRKCRWPLYGDPITFAPFKISCENEQ-ARTDYFIRTLLEFQN 184

Qy 183 ESRVYQLQYMSWDRGVSPDRLMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVLCTV 242
 Db 185 ESRLYQHYVNWPDHVPSSFDSDILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244

Qy 243 DYVRQLLLTQMIPPDFSLFDVVLKMRKORPAAVQTEQYRFLYHTVAQMFCSLTQ----- 297
 Db 245 DYTWNLLKAGKIPPEFNVFNLIQEMRTQRHSVQTKQYELVHRAIAQLFEKQLQYIEIH 304

Qy 298 -----IPRP----- 297

Db 305 GAQKIRGNEITTTGTVSSIDSEKQSPPKPPRTRCLVEGDAKEBILQPPHPVPPPI 364

Qy 298 -----NASP----- 301

Db 365 LTPSPPSAFPTVTWQDSRYHPKPVLLHMASPEQHPADLNRSYDKSADQWKGKSESAIEH 424

Qy 302 -----HYQNIKENCAPLYDDALFLRT--PQA 325

Db 425 IDKKLERNLSPEIKKVPLOQPKSFDGNTLLNRGHAIKIKSASSSVVD-----RTSKPQE 479

Qy 326 LLA-----PGGVLRSI- 340

Db 480 LSAGALKVDDVQNSCADCSAAHSHRAAESSESQNSHTPPRPDCLPLDKKGHTVWSLH 539

Qy 341 -----SVFGSPGHAMADTY-----ABEQKR----- 360

Search completed: August 17, 2004, 20:50:05
 Job time : 50 secs

Db 540 GPNATPVDPSPDGKSPDNHSQTLKTVSSSTPNSTAEEEAHDLTEHHNSSPLLKAPLSFTN 599
 Qy 361 -----GAPAGAGSGTQTGTGTOA-----RSAEEAPLYSKYVTPR----- 393
 Db 600 PLHSDDMHSDGGSSDGAVTNRKTSISTASATVSPASSAESACHRRVLEPMSTARQEVAGTP 659
 Qy 394 ---AORPCAHAEADARGTLPGRVP----- 413
 Db 660 HSGAEKADADVSEBSPPPLPERTPESFVLADMPVPEWHELPNQEMSQRESEGLTTSGNE 719
 Qy 414 -----ADQSPAGSGAYEDVA--GGAQTGGLGFNLRIGRPKGPRDPPPAEW 456
 Db 720 KHDAGGIHTEASADSPAFSDKQDQITKSPAENVTDIGFNGRCGPKGPREPPSEWT 775

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:40:39 ; Search time 17 Seconds
(without alignments)
2591.513 Million cell updates/sec

Title: US-10-087-993a-36

Perfect score: 2424
Sequence: 1 MSRLDSARSLERLEARGG.....NLRIKPKGRDPPEAWTRV 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.78.*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	755.5	31.2	802	1 B44390	protein-tyrosine-p
2	710	29.3	773	1 JH0609	protein-tyrosine-p
3	709	29.2	780	1 JCI368	protein-tyrosine-p
4	705.5	29.1	382	1 S48748	protein-tyrosine-p
5	705	29.1	775	2 S55345	protein-tyrosine-p
6	491.5	20.3	1118	1 A49724	protein-tyrosine-p
7	475.5	19.6	595	1 A44390	protein-tyrosine-p
8	474	19.6	1711	1 A55148	protein-tyrosine-p
9	463	19.1	595	1 S20825	protein-tyrosine-p
10	462	19.1	926	1 A41105	protein-tyrosine-p
11	453	18.7	593	1 JN0805	protein-tyrosine-p
12	453	18.7	593	2 JC5167	protein-tyrosine-p
13	451	18.6	585	2 A46209	protein-tyrosine-p
14	449	18.5	597	1 A53593	protein-tyrosine-p
15	448	18.5	521	1 A44267	protein-tyrosine-p
16	448	18.5	913	1 A41109	protein-tyrosine-p
17	444	18.3	595	1 A55651	protein-tyrosine-p
18	442	18.2	694	2 A53978	protein-tyrosine-p
19	441	18.2	597	2 B53978	protein-tyrosine-p
20	435	17.9	1337	1 T38670	protein-tyrosine-p
21	431	17.8	398	2 T08716	protein-tyrosine-p
22	430.5	17.8	435	1 TPHUN1	protein-tyrosine-p
23	430	17.7	593	1 A42690	protein-tyrosine-p
24	429.5	17.7	593	2 S17671	protein-tyrosine-p
25	428	17.7	624	2 T19630	hypothetical prote
26	428	17.7	1026	2 T19631	protein-tyrosine-p
27	426.5	17.6	802	1 A36065	protein-tyrosine-p
28	424.5	17.5	1437	2 T31093	probable protein-t
29	424.5	17.5	2490	1 A54971	protein-tyrosine-p

30	424	17.5	1301	1 A41622	protein-tyrosine-p
31	423.5	17.5	829	1 A47373	protein-tyrosine-p
32	423	17.5	360	1 JH0692	protein-tyrosine-p
33	421.5	17.4	1238	2 S68700	Hppp beta-like tyr
34	421.5	17.4	2294	2 I67630	protein-tyrosine-p
35	421.5	17.4	2466	2 I67629	protein-tyrosine-p
36	421	17.4	1200	2 T43148	probable protein-t
37	420	17.3	1898	2 S46216	leukocyte antigen-
38	420	17.3	2051	2 T30938	receptor tyrosine
39	419.5	17.3	1188	1 A57064	protein-tyrosine-p
40	419.5	17.3	1216	2 S60613	protein-tyrosine-p
41	419.5	17.3	1997	1 S12050	protein-tyrosine-p
42	419	17.3	1442	1 B48148	protein-tyrosine-p
43	419	17.3	1445	1 A48148	protein-tyrosine-p
44	418.5	17.3	405	2 I49372	protein-tyrosine-p
45	418.5	17.3	1897	1 TDHULK	leukocyte antigen-

ALIGNMENTS

RESULT 1

B44390
N:Alternate names: protein-tyrosine-phosphatase PEP
C:Species: Mus musculus (house mouse)
C>Date: 03-May-1994 #sequence_revision 26-May-1994 #text_change 11-Jun-1999
C:Accession: B44390; S71952; S27876
R:Matthews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L.
Mol. Cell. Biol. 12, 2396-2405, 1992
A:Title: Characterization of hematopoietic intracellular protein tyrosine phosphatases: c and threonine-rich sequences.
A:Reference number: A44390; MUID:92236615; PMID:1373816
A:Accession: B44390
A:Molecule type: mRNA
A:Residues: 1-802 <MA>
A:Cross-references: GB:M90388; NID:g200522; PIDN:AAA39994.1; PID:g200523
R:Cloutier, J.F.; Veillette, A.
EMBO J. 15, 4903-4918, 1996
A:Title: Association of inhibitory tyrosine protein kinase p50(csk) with protein tyrosine phosphatases: c and threonine-rich sequences.
A:Reference number: S71952; MUID:97045099; PMID:8890164
A:Accession: S71952
A:Molecule type: mRNA
A:Residues: 495-789 <CLO>
C:Comment: This protein is found primarily in hematopoietic tissues.
C:Genetics:
C:Gene: 70zpep
C:Complex: physically associates with inhibitory tyrosine protein kinase Csk; interaction
C:Function:
A:Description: probably an effector and/or regulator of tyrosine protein kinase csk in T.
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 8; protein-tyrosine-phosphatase
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:54-278/Domain: protein-tyrosine-phosphatase homology <PIP>
F:497-802/Region: glutamic acid/proline/serine/threonine-rich
F:613-621/Region: proline-rich
F:688-695/Region: proline-rich
F:227/Active site: Cys (phosphocysteine intermediate) #status predicted
F:233/Binding site: substrate phosphate (Arg) #status predicted

Query Match	31.2%	Score	755.5	DB	1	Length	802
Best Local Similarity	44.0%	Pred. No.	2e+47				
Matches	161	Conservative	55	Mismatches	119	Indels	31
Gaps	7						
Qy	27	AGEPSDIOACGAADKADGVCSTAGSRPENVKRYKDVLPYDQTRVLSLLQEBGSDY	86				
Db	25	ASEFPLKRSQTKYKADKIYFTVAQRPNKKRYKDVLPYDQTRVLSLLQEBGSDY	84				
Qy	87	INGNFIRGVGDSLAYIATQGPLPHTLLDFWRLWFEVGVKVIILMACREIENGKRCERYA	146				
Db	85	INASIKGVYGPAYATQGPLSTLLDFWRMIWEYRILVIMACMEFEMGKKCERYA	144				
Qy	147	QEQE-PLQTGLFCITLKEKWLNEDIMLTLLKVFQKESRSVYQLQYNSWDRGVPSDD	205				

A:Title: Mutations at the murine motheaten locus are within the hematopoietic cell prote
A:Reference number: 152816; MUID:93313972; PMID:8324828
A:Accession: I65741
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 334-353, 359-382 <SHU1>
A:Cross-references: GB:963803; NID:9388449
A:Note: deletion mutation
A:Accession: 152816
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 350-358, 'EGOSPFLTTFSSLVVQVHTQ', 359-366 <SHU2>
A:Cross-references: GB:963763; NID:9388447
A:Note: insertion mutation
A:Accession: I65740
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 34-76, 'VPRPIHWAGGVTAAGQGRALD', <SHU3>
A:Cross-references: GB:963764; NID:9388450
A:Note: frameshift mutation
R:Yeung, Y.G.; Berg, K.L.; Poxley, F.J.; Angeletti, R.H.; Stanley, E.R.
J. Biol. Chem. 267, 23447-23450, 1992
A:Title: Protein tyrosine phosphatase-1C is rapidly phosphorylated in tyrosine in macroph
A:Reference number: A45143; MUID:93054686; PMID:1385421
A:Accession: A45143
A:Status: preliminary
A:Molecule type: protein
A:Residues: 137-139, 'X', 141-143, 'X', 145-151 <YE>
A:Experimental source: BAC1.2F5 macrophage
A:Note: sequence extracted from NCBI backbone (NCBIP:118519)
A:Accession: B45143
A:Status: preliminary
A:Molecule type: protein
A:Residues: 54-56, 'X', 58, 'X', 60-61, 'X', 63-68 <YE2>
A:Experimental source: BAC1.2F5 macrophage
A:Note: sequence extracted from NCBI backbone (NCBIP:118518)
C:Comment: This protein is found primarily in hematopoietic tissues.
C:Genetics:
A:Gene: me/HCPH; motheaten
C:Function:
A:Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to release phosphate
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat
F:4-98/Domain: SH2 homology <SH2A>
F:110-211/Domain: SH2 homology <SH2B>
F:265-521/Domain: phosphatase catalytic domain #status predicted <PHP>
F:270-504/Domain: protein-tyrosine-phosphatase homology <PTP>
F:453/Active site: Cys (phosphocysteine intermediate) #status predicted
F:455/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.6%; Score 475.5; DB 1; Length 595;
Best Local Similarity 36.2%; Pred. No. 4.4e-27;
Matches 106; Conservative 53; Mismatches 105; Indels 29; Gaps 8;

Qy 22 EGAVLAG---EFSDIQCSAAWKADGVCSTVAGSRPENVRKNRYKDVLPDQTRVLSLL 78
Db 237 EDTAKAGFWBFEFSLQ---KQEVNKLHQLEGGQRPNKKNRYKNILPFDHRSVIL--- 289
Qy 79 QEEGH-----SDYINGNFIRGV-----DGLAVIATQGLPHTLDFWRLVWFGVKVI 127
Db 290 --QGEDSNIPGSDIYNANYVKNQLLGDENSRTYIASQGLDATVDFQWMAQENTRVI 347
Qy 128 LMACRETENGKRCERYWAEQEPLOTGLFCITILKEKWLNEDIMLTKVTFQKES--- 184
Db 348 VMTTREVKEGKNCVYWPVEGTQVRYGLYSVTNSRHDTAE-YKLRTLQISPLDNGDLV 406
Qy 185 SVVQLOVMSWPDGRGVPSSPDHMLAWEEARRLOGSGPE--PLCVHCSAGCGRTGLVCTV 242
Db 407 REIWHYQLSWPDGRGVSEPGCVLSFLDQINQROESLPHAGPIIVHCSAGIGRTIIVI 466
Qy 243 DYVRQLLTQIMPPDFSLDFVYLKMKRQPPAAVQTEBEQYRFLXHTVAMQFCST 295
Db 467 DMLMESISTKGLDCDIDIQKTIQWVRAQRSGMWQTEAQYKFIYVIAQFIETT 519

RESULT 8

A55148
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat
N:Alternate names: OST-PTP; osteostecticular protein-tyrosine-phosphatase
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A55148
R:Mauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, J.E.
J. Biol. Chem. 269, 30659-30667, 1994
A:Title: Identification of a hormonally regulated protein tyrosine phosphatase associated
A:Reference number: A55148; MUID:95074080; PMID:7527035
A:Accession: A55148
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-1711 <MAU>

A:Cross-references: GB:L36884
C:Comment: The sequence contains ten fibronectin type III repeats and two protein-tyrosin
C:Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin type III repe
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prote
F:1-18/Domain: signal sequence #status predicted <SG>
F:19-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status predicted <MA
F:1174-1398/Domain: protein-tyrosine-phosphatase homology <PTP1>
F:1350/Active site: Cys (phosphocysteine intermediate) #status predicted
F:1356/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.6%; Score 474; DB 1; Length 1711;
Best Local Similarity 39.9%; Pred. No. 2.2e-26;
Matches 114; Conservative 35; Mismatches 111; Indels 26; Gaps 8;

Qy 10 SFLELRAGRGREGAVLAGFSDIQCSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYD 69

Db 1134 SFRQSYEAKSAHAHQTFQFEELKEVKDQ-----PRLAEHPDNIKNRYPHVLPYD 1187

Qy 70 QTRVLSLLQEEGHSDYINGNFIRVDGSLAYIATQGLPHTLDFWRLVWFGVKVILM 129

Db 1188 HSRVLTQLPGEPHSDYINANFPGYSHTQIIATQGLPKKTLEDFWRLVWQQVHVIM 1247

Qy 130 ACRETENGKRCERYWAEQEPLOTGLFCITILKE---KWLNEDIMLTKVTFQKESR 185

Db 1248 LVGVNENGLCEHYWPANSFVTHGHTIHLAEPDEWTRREFQLQ--HGTEQXQ-R 1304

Qy 186 SVYQLQYMSWPDGRGVPSSPDHMLAMV---BEARRLOGSGPEPLCVHCSAGCGRTGLVCT 241

Db 1305 RVKQLQFTWPDHSVPEAFSSLLAFVELVQEQVQATQKG--PILVHCSAGVGRGT--- 1359

Qy 242 VDYYRQLLTQIMPPD--FSULFDVVLKMKRQPPAAVQTEBEQYRELY 285

Db 1360 --FVALLRLRLQLEBEKVADVNTVYILRLHRLPLMIQTLSTQYIFLH 1403

RESULT 9

S20825

protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN6, nonreceptor type 6 [validated] - human
N:Alternate names: hematopoietic cell phosphatase HCP; protein-tyrosine-phosphatase 1C; I
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 08-Feb-1996 #text_change 21-Jun-2002

C:Accession: B42031; A38189; S20825; S17234; S20837

R:Yi, T.L.; Cleveland, J.L.; Ihle, J.N.

Mol. Cell. Biol. 12, 836-846, 1992

A:Title: Protein tyrosine phosphatase containing SH2 domains: characterization, preferen
A:Reference number: A42031; MUID:92123209; PMID:1732748

A:Accession: B42031

A:Molecule type: mRNA

A:Residues: 1-595 <YII>

A:Cross-references: GB:M74093

A:Experimental source: T-lymphoid cell line

A:Note: sequence extracted from GenBank

R:Plutsky, J.; Neel, B.G.; Rosenberg, R.D.

Proc. Natl. Acad. Sci. U.S.A. 89, 1123-1127, 1992

A:Title: Isolation of a src homology 2-containing tyrosine phosphatase.

A:Reference number: A38189; MUID:92141214; PMID:1736296

A:Accession: A38189
 A:Molecule type: mRNA
 A:Residues: 1-85, 'V', 87-595 <PLU>
 A:Cross-references: GB:M77273; NID:g338079; PIDN:AAA36610.1; PID:g338080
 A:Note: sequence extracted from NCBI backbone (NCBIN:79619, NCBI:P:79620)
 R:Shen, S.H.; Bastien, L.; Posner, B.I.; Chretien, P.
 Nature 353, 868, 1991
 A:Title: Corrigendum: A protein-tyrosine phosphatase with sequence similarity to the SH2
 A:Reference number: S20825
 A:Accession: S20825
 A:Molecule type: mRNA
 A:Residues: 1-'LSRG', 4-595 <SH>
 A:Cross-references: EMBL:X62055; NID:g35781; PIDN:CAA43982.1; PID:g35782
 R:Shen, S.H.; Bastien, L.; Posner, B.I.; Chretien, P.
 Nature 352, 736-739, 1991
 A:Title: A protein-tyrosine phosphatase with sequence similarity to the SH2 domain of th
 A:Reference number: S17234; MUID:91343005; PMID:1652101
 A:Accession: S17234
 A:Molecule type: mRNA
 A:Residues: 1-'LSRG', 4-589, 'VPSRGSRCCPQVAMPQP' <SH2>
 A:Experimental source: breast carcinoma cells
 A:Note: sequence revised in reference S20805
 C:Genetics:
 A:Gene: GDB:PTPN6
 A:Cross-references: GDB:131389; OMIM:176883
 A:Map position: 12p13-12p13
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosphat
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:4-98/Domain: SH2 homology <SH2A>
 F:110-211/Domain: SH2 homology <SH2B>
 F:265-521/Domain: phosphatase catalytic domain #status predicted <P>
 F:270-504/Domain: protein-tyrosine-phosphatase homology <P>
 F:453/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:459/Binding site: substrate phosphate (Arg) #status predicted
 Query Match 19.1%; Score 463; DB 1; Length 595;
 Best Local Similarity 32.9%; Pred. No. 3.6e-26;
 Matches 112; Conservative 56; Mismatches 110; Indels 62; Gaps 10;
 QY 22 EGAVIAG---EFSDIQACSAANKADGVCSTVAGSRPNKRYKDVLPDQTRVLSL 78
 DB 237 EDTAKAGFEFESLQ---KQEVNKLHRLGORPENKGNKRYKNLPPDHSRVIL--- 289
 QY 79 QEEGH-----SDYINGNFRGV-----DGLAYIATQGLPHTLLDFWLVWFEVGVKY 127
 DB 290 --QGRDNIPEGSDYINANYIKNQLLGDENAKTYIASQGLCATVNDVFWQMAQENSRVI 347
 QY 128 LMACREIENGKRCERYAQOEPLQTGLFCITLKEKWLNEIMLRTLKVTFOKES--- 184
 DB 348 VMTTREVKEGRNKCVPYVPGVQRAYGVPYVINCSEHDTTE-YKLTQLQVSLDNGDLI 406
 QY 185 RSVYQLQMWDPGRVSPDPHMLAMVEEARLQGSPE--PLCVHCSACGRTGVLCTV 242
 DB 407 REIHHYQLSWPDHGVSEPGVLSFLDQINQKESLPHAGPIIVHVCAGIGSTGTIIVI 466
 QY 243 DYVQLLLTQWIPDFSLDFVLMKRRQPAAVQTEQVRFVHTVAQMFCST----- 295
 DB 467 DMLNENISTKGLDCDDIDIKTIQWVRAQRSGMVQTEAQYKFIYVAQAQFIETTKKLEVL 526
 QY 296 -----LQNA-----SPHYQNIKEN 309
 DB 527 QSQKGQSEYCNITYPPAMKNAAKASRTSGKHKEDVYEN 566
 RESULT 10
 A41105
 protein-tyrosine-phosphatase (BC 3.1.3.48) PTPN4, nonreceptor type 4 [validated] - human
 N:Alternate names: PTPase MEG
 C:Species: Homo sapiens (man)
 C:Date: 20-Mar-1992 #sequence_revision 02-May-1994 #text_change 21-Jun-2002
 A:Accession: A41105
 R:Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.
 Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991
 A:Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-ty
 A:Reference number: A41105; MUID:91288564; PMID:1648233
 A:Accession: A41105
 A:Molecule type: mRNA
 A:Residues: 1-926 <GUA>
 A:Cross-references: GB:M68941; NID:g190747; PIDN:AAA36530.1; PID:g190748
 A:Experimental source: megakaryocytes, cell line MEG-10
 C:Genetics:
 A:Gene: GDB:PTPN4
 A:Cross-references: GDB:131387; OMIM:176878
 A:Map position: 9q31-9q31
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; ph
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:523-597/Domain: GLGF domain homology <GLG>
 F:679-900/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:852/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:858/Binding site: substrate phosphate (Arg) #status predicted
 Query Match 19.1%; Score 462; DB 1; Length 926;
 Best Local Similarity 37.6%; Pred. No. 7.5e-25;
 Matches 106; Conservative 47; Mismatches 107; Indels 22; Gaps 9;
 QY 17 ARGGRGAVLAGFSDIQACSAANKADGVCSTVAGSRPNKRYKDVLPDQTRVLS 76
 DB 647 AEGITGTFLT-QFDQLYR-----KFGMTWNSCA-KLPQNIKRNRYRDISPYDATRVIL- 698
 QY 77 LLQBEHSDYINGNFRIGVDSGLA---YIATQGLPHTLLDFWLVWFEVGVKILMACR 132
 DB 699 ---KGNEDYINANYINWEIPSSIIINQYIACQGLPHTCTDFWQMTWEGSSMVVMLTT 754
 QY 133 EIENGRKRCERYAQOEPLQTGLFCITLKEKWLNEIMLRTLKVTFOK--ESRSYVOL 190
 DB 755 QVERGRVKCHOVPEPTGSSSYGYQVTCHEEG-NTAYIFRKMTLFNQKESRPTQI 813
 QY 191 QYMSWPDGRVSPDPHMLAMVEEARLQGSPEPLCVHCSACGRTGVLCTVDYVROLLL 250
 DB 814 QYIAMPDHGVDDSSDFLDFVCHVRNKRAGKEEPVTVHCSAGIGRTGVLITME--TAMCL 871
 QY 251 TQMTIPPSPFLDVVLKMKRRQPAAVQTEQVRFVHTVAQM 292
 DB 872 IECNQVYVPL-DIVRTWRDORAMMIQTPSQYRFVCEAILKYV 912
 RESULT 11
 UN0805
 protein-tyrosine-phosphatase (BC 3.1.3.48) PTPN11, nonreceptor type 11 [validated] - huma
 N:Alternate names: BPTP-3; protein-tyrosine-phosphatase SHP-2; PTP1D; PTP2C; SH-PTP2; SH-
 C:Species: Homo sapiens (man)
 C:Date: 10-Mar-1994 #sequence_revision 19-May-1994 #text_change 21-Jun-2002
 C:Accession: UN0805; A46210; A47386; A47244; S27398; C44929; S31767
 R:Bastien, L.; Ranachandran, C.; Liu, S.; Adam, M.
 Biochem. Biophys. Res. Commun. 196, 124-133, 1993
 A:Title: Cloning, expression and mutational analysis of SH-PTP2, human protein-tyrosine p
 A:Reference number: UN0805; MUID:94029983; PMID:8216283
 A:Accession: UN0805
 A:Molecule type: mRNA
 A:Residues: 1-593 <BAS>
 A:Cross-references: GB:L07527; NID:g292406; PIDN:AAA17022.1; PID:g292407
 R:Voegel, W.; Lammers, R.; Huang, J.; Ullrich, A.
 Science 259, 1611-1614, 1993
 A:Title: Activation of a phosphotyrosine phosphatase by tyrosine phosphorylation.
 A:Reference number: A46210; MUID:93206095; PMID:7681217
 A:Accession: A46210
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-593 <VO>
 A:Cross-references: EMBL:X70766; NID:g35783; PIDN:CAA50045.1; PID:g35784
 A:Experimental source: SK-BR-3 mammary carcinoma cells
 A:Note: sequence extracted from NCBI backbone (NCBI:P:127775)
 R:Ahmad, S.; Banville, D.; Zhao, Z.; Fischer, E.H.; Shen, S.H.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2197-2201, 1993
 A:Title: A widely expressed human protein-tyrosine phosphatase containing src homology 2

A:Reference number: A47386; MUID:93211929; PMID:7681589
A:Accession: A47386
A:Molecule type: mRNA
A:Residues: 1-593 <AHM>
A:Experimental source: umbilical cord
A:Note: sequence extracted from NCBI backbone (NCBIN:128129, NCBIPI:128131)
R:Freeman Jr., R.M.; Plutzky, J.; Neel, B.G.
Proc. Natl. Acad. Sci. U.S.A. 89, 11239-11243, 1992
A:Title: Identification of a human src homology 2-containing protein-tyrosine-phosphatase
A:Reference number: A47244; MUID:93087502; PMID:1280823
A:Accession: A47244
A:Molecule type: mRNA
A:Residues: 1-593 <PRE>
A:Cross-references: GB:103535; NID:9338081; PIDN:AAA36611.1; PID:9338082
A:Note: sequence extracted from NCBI backbone (NCBIN:119760, NCBIPI:119761)
R:Adachi, M.; Sekiya, M.; Miyachi, T.; Matsuno, K.; Hinoda, Y.; Imai, K.; Yachi, A.
FEBS Lett. 314, 335-339, 1992
A:Title: Molecular cloning of a novel protein-tyrosine phosphatase SH-PTP3 with sequence homology to SH-PTP2
A:Reference number: S27398; MUID:93106179; PMID:1281790
A:Accession: S27398
A:Molecule type: mRNA
A:Residues: 1-534; R:536-547, P:549-593 <AD2>
A:Cross-references: DDBJ:D13540; NID:9220071; PIDN:BA02740.2; PID:94519425
R:Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yachi, A.
Cancer Res. 52, 737-740, 1992
A:Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.
A:Reference number: A44929; MUID:92119637; PMID:1370651
A:Accession: C44929
A:Molecule type: mRNA
A:Residues: 1-370, 370-460 <ADA>
A:Cross-references: GB:578088; NID:9243547; PIDN:AAB21148.1; PID:9243548
A:Experimental source: pre-B cell NALM-6
A:Note: sequence extracted from NCBI backbone (NCBIN:78088, NCBIPI:78089)
A:Note: the authors did not report the entire codon for residue 92
A:Comment: This ubiquitous enzyme plays a critical role in regulating physiological cell growth and differentiation
C:Genetics:
A:Gene: PTPN11
A:Cross-references: GDB:137093; OMIM:176876
A:Map position: 12q24.1-12q24.1
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosphatase
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:6-100/Domain: SH2 homology <SH2a>
F:112-214/Domain: SH2 homology <SH2b>
F:273-510/Domain: protein-tyrosine-phosphatase intermediate
F:459/Active site: Cys (phosphocysteine intermediate) #status predicted
F:465/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.7%; Score 453; DB 1; Length 593;
Best Local Similarity 33.8%; Pred. No. 2e-25;
Matches 119; Conservative 53; Mismatches 126; Indels 54; Gaps 12;
QY 1 MSRLDSARSFLERLEARGREGAVLA-----GEFSDI--QACSAANKADGVCS 47
DB 212 LKQPLNTRINAABIESR-VRELSKLAETTDVKVQGFWEFEETLQQECKLLY-----S 264
QY 48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLQEEGH-----SDYINGNFI-----RG 94
DB 265 RKEGQRENKNRYKNILPFDHTRVVL-----HDGDPNEPVSVDYINANIIMPETKCNN 320
QY 95 VDGLSAYATQGPLPHTLLDFWRLVWVEFGVKVILMACREIENGRCRCERYWAQEQELQ 154
DB 321 SKPKKSYIATQGLQNTVNDWFWMVFQENSRIVMTTKEVERGSKCKVYWPDEYSLKEY 380
QY 155 GLFCITLKEKWLNEDIMRLTKVTFQKE---SRSVYQLQYMSWPDGVPSSPDHMLAMV 211
DB 381 GVMVRNVKES-AAHDYTLRELKLSKVGGQNTERTVQYHFTWPDHGVSDPGGVLDLFL 439
QY 212 BEARLQSGSP--PLCVHCSAGCGRTGVLCTVDYVRQLLTQMIPPDFSLFDVVLKMRK 269
DB 440 EEVHHKQESIMDAGPVVHCSAGIGRTGTFIVIDLIDIREKGVDCDIDVPKTIQMVRS 499
QY 270 QRPAAVQTEEQRYFLYHTVAQMFCSLTQ-----NASPHYQNIK 307
DB 500 QRSQMVQTEAQRYFYIMAV-QHYIETLQRIIEEQSKRKRGHEYTNIK 546
Query Match 18.7%; Score 453; DB 2; Length 593;
Best Local Similarity 33.9%; Pred. No. 2e-25;
Matches 118; Conservative 53; Mismatches 123; Indels 54; Gaps 12;
QY 1 MSRLDSARSFLERLEARGREGAVLA-----GEFSDI--QACSAANKADGVCS 47
DB 212 LKQPLNTRINAABIESR-VRELSKLAETTDVKVQGFWEFEETLQQECKLLY-----S 264
QY 48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLQEEGH-----SDYINGNFI-----RG 94
DB 265 RKEGQRENKNRYKNILPFDHTRVVL-----HDGDPNEPVSVDYINANIIMPETKCNN 320
QY 95 VDGLSAYATQGPLPHTLLDFWRLVWVEFGVKVILMACREIENGRCRCERYWAQEQELQ 154
DB 321 SKPKKSYIATQGLQNTVNDWFWMVFQENSRIVMTTKEVERGSKCKVYWPDEYSLKEY 380
QY 155 GLFCITLKEKWLNEDIMRLTKVTFQKE---SRSVYQLQYMSWPDGVPSSPDHMLAMV 211
DB 381 GVMVRNVKES-AAHDYTLRELKLSKVGGQNTERTVQYHFTWPDHGVSDPGGVLDLFL 439
QY 212 BEARLQSGSP--PLCVHCSAGCGRTGVLCTVDYVRQLLTQMIPPDFSLFDVVLKMRK 269
DB 440 EEVHHKQESIMDAGPVVHCSAGIGRTGTFIVIDLIDIREKGVDCDIDVPKTIQMVRS 499
QY 270 QRPAAVQTEEQRYFLYHTVAQMFCSLTQ-----NASPHYQNIK 307
DB 500 QRSQMVQTEAQRYFYIMAV-QHYIETLQRIIEEQSKRKRGHEYTNIK 546

RESULT 13

A46209

protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 11 - mouse
N:Alternate names: SH-PTP2; SH2-containing phosphotyrosine phosphatase Syp
C:Species: Mus musculus (house mouse)
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Apr-1998
A:Accession: A46209
R:Feng, G.S.; Hui, C.C.; Pawson, T.
Science 259, 1607-1611, 1993
A:Title: SH2-containing phosphotyrosine phosphatase as a target of protein-tyrosine kinase
A:Reference number: A46209; MUID:93206094; PMID:8096088
A:Accession: A46209

A:Reference number: A47386; MUID:93211929; PMID:7681589
A:Accession: A47386
A:Molecule type: mRNA
A:Residues: 1-593 <AHM>
A:Experimental source: umbilical cord
A:Note: sequence extracted from NCBI backbone (NCBIN:128129, NCBIPI:128131)
R:Freeman Jr., R.M.; Plutzky, J.; Neel, B.G.
Proc. Natl. Acad. Sci. U.S.A. 89, 11239-11243, 1992
A:Title: Identification of a human src homology 2-containing protein-tyrosine-phosphatase
A:Reference number: A47244; MUID:93087502; PMID:1280823
A:Accession: A47244
A:Molecule type: mRNA
A:Residues: 1-593 <PRE>
A:Cross-references: GB:103535; NID:9338081; PIDN:AAA36611.1; PID:9338082
A:Note: sequence extracted from NCBI backbone (NCBIN:119760, NCBIPI:119761)
R:Adachi, M.; Sekiya, M.; Miyachi, T.; Matsuno, K.; Hinoda, Y.; Imai, K.; Yachi, A.
FEBS Lett. 314, 335-339, 1992
A:Title: Molecular cloning of a novel protein-tyrosine phosphatase SH-PTP3 with sequence homology to SH-PTP2
A:Reference number: S27398; MUID:93106179; PMID:1281790
A:Accession: S27398
A:Molecule type: mRNA
A:Residues: 1-534; R:536-547, P:549-593 <AD2>
A:Cross-references: DDBJ:D13540; NID:9220071; PIDN:BA02740.2; PID:94519425
R:Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yachi, A.
Cancer Res. 52, 737-740, 1992
A:Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.
A:Reference number: A44929; MUID:92119637; PMID:1370651
A:Accession: C44929
A:Molecule type: mRNA
A:Residues: 1-370, 370-460 <ADA>
A:Cross-references: GB:578088; NID:9243547; PIDN:AAB21148.1; PID:9243548
A:Experimental source: pre-B cell NALM-6
A:Note: sequence extracted from NCBI backbone (NCBIN:78088, NCBIPI:78089)
A:Note: the authors did not report the entire codon for residue 92
A:Comment: This ubiquitous enzyme plays a critical role in regulating physiological cell growth and differentiation
C:Genetics:
A:Gene: PTPN11
A:Cross-references: GDB:137093; OMIM:176876
A:Map position: 12q24.1-12q24.1
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosphatase
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:6-100/Domain: SH2 homology <SH2a>
F:112-214/Domain: SH2 homology <SH2b>
F:273-510/Domain: protein-tyrosine-phosphatase intermediate
F:459/Active site: Cys (phosphocysteine intermediate) #status predicted
F:465/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.7%; Score 453; DB 1; Length 593;
Best Local Similarity 33.8%; Pred. No. 2e-25;
Matches 119; Conservative 53; Mismatches 126; Indels 54; Gaps 12;

QY 1 MSRLDSARSFLERLEARGREGAVLA-----GEFSDI--QACSAANKADGVCS 47
DB 212 LKQPLNTRINAABIESR-VRELSKLAETTDVKVQGFWEFEETLQQECKLLY-----S 264
QY 48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLQEEGH-----SDYINGNFI-----RG 94
DB 265 RKEGQRENKNRYKNILPFDHTRVVL-----HDGDPNEPVSVDYINANIIMPETKCNN 320
QY 95 VDGLSAYATQGPLPHTLLDFWRLVWVEFGVKVILMACREIENGRCRCERYWAQEQELQ 154
DB 321 SKPKKSYIATQGLQNTVNDWFWMVFQENSRIVMTTKEVERGSKCKVYWPDEYSLKEY 380
QY 155 GLFCITLKEKWLNEDIMRLTKVTFQKE---SRSVYQLQYMSWPDGVPSSPDHMLAMV 211
DB 381 GVMVRNVKES-AAHDYTLRELKLSKVGGQNTERTVQYHFTWPDHGVSDPGGVLDLFL 439
QY 212 BEARLQSGSP--PLCVHCSAGCGRTGVLCTVDYVRQLLTQMIPPDFSLFDVVLKMRK 269
DB 440 EEVHHKQESIMDAGPVVHCSAGIGRTGTFIVIDLIDIREKGVDCDIDVPKTIQMVRS 499
QY 270 QRPAAVQTEEQRYFLYHTVAQMFCSLTQ-----NASPHYQNIKENCA 311
DB 500 QRSQMVQTEAQRYFYIMAV-QHYIETLQRIIEEQSKRKRGHEYTNIK 546

A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-585 <FEN>
 A>Note: sequence extracted from NCBI backbone (NCBIP:127770)
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosphatase
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:6-100/Domain: SH2 homology <SH2A>
 F:112-214/Domain: SH2 homology <SH2B>
 F:273-514/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:463/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:469/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.6%; Score 451; DB 2; Length 585;
 Best Local Similarity 31.0%; Pred. No. 2,7e-25;
 Matches 128; Conservative 59; Mismatches 142; Indels 84; Gaps 15;

QY 1 MSRLDSARSFLERLARGREGAVLA-----GFSDI--QACSAANKADGVCS 47
 DB 212 LKQPLNTRINAAIESR-VRELSKLAETTDKVKQGFWEFETLQOQCKLLY-----S 264
 QY 48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLQEGH-----SDYINGNFI-----RG 94
 DB 265 RKEGQRQENKNRYKNILPFDHTRVVL---HGDNPVPVSYINANIIMPEFETKCNN 320
 QY 95 VDGLAYIATQGPLPHTLLDFWLVWFGVKVILMACREIENGRCRCERYWAOEPLQT 154
 DB 321 SKPKSYIATQGCQLQNTVDFWVFOENSRVIMTTKEVERGSKCKVYWPDEYALKEY 380
 QY 155 GLPCTILIKEKWLNEDIMRLTKVTFOKES-----RSVYQLOYMSWDRGVPSSPDHM 207
 DB 381 GVMVRNVKES-AAHDYTLRELKLSKVGQALLQNTERTVQYHFTWPDHGVSPDPGV 439
 QY 208 LAMVEEARLQGS--GPEPLCVHCSAGCGRTGVLTVDYVQRLLTQMIQPPDFSLFDVVL 265
 DB 440 LDFLEEVHVKQESIVDAGPVVHCSAGIGRTGTFIVIDLIREKGVDCDDIVPKTIQ 499
 QY 266 KMRQORPAAVOTEQRYFLYHTVAQMFCSLTQ-----NASPHYQNIKENCAPLYD 315
 DB 500 MVRQSRGVMQTEAQRYFIYNAV-QHYETLQRIEIEQSKRGKHEYNIKSS---LVD 552
 QY 316 DALFLRTPOALLAIPRPPGVLRIS 341
 DB 553 GELGYTTRV-----GCGHVSVP--MDEVGGWVEGLGT 585

RESULT 14
 A53593
 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 11 - rat
 N:Alternate names: pTase L1
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A53593; S29281
 R:Mei, L.; Doherty, C.A.; Haganir, R.L.
 J. Biol. Chem. 269, 12254-12262, 1994
 A>Title: RNA splicing regulates the activity of a SH2 domain-containing protein tyrosine
 A:Reference number: A53593; MUID:94216346; PMID:7512964
 A:Accession: A53593
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-597 <MEI>
 A:Cross-references: GB:U05963; NID:G458332; PIDN:AAAL1913.1; PID:G458333
 R:Hiraga, A.; Munakata, H.; Hata, K.; Suzuki, Y.; Tsukui, S.
 Eur. J. Biochem. 209, 195-206, 1992
 A>Title: Purification and characterization of a rat liver protein-tyrosine phosphatase
 A:Reference number: S29281; MUID:93011127; PMID:1382983
 A:Accession: S29281
 A:Molecule type: protein
 A:Residues: 24-31;36-54;56-89;100-103;X',113-120;132-155;179-198;214-233;24
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosphatase
 C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosine
 F:6-100/Domain: SH2 homology <SH2A>
 F:112-214/Domain: SH2 homology <SH2B>
 F:273-514/Domain: protein-tyrosine-phosphatase homology <PTP>

F:463/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:469/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.5%; Score 449; DB 1; Length 597;
 Best Local Similarity 32.4%; Pred. No. 3.9e-25;
 Matches 125; Conservative 58; Mismatches 141; Indels 62; Gaps 14;

QY 1 MSRLDSARSFLERLARGREGAVLA-----GFSDI--QACSAANKADGVCS 47
 DB 212 LKQPLNTRINAAIESR-VRELSKLAETTDKVKQGFWEFETLQOQCKLLY-----S 264
 QY 48 TVAGSRPENVRKNRYKDVLPYDQTRVILSLQEGH-----SDYINGNFI-----RG 94
 DB 265 RKEGQRQENKNRYKNILPFDHTRVVL---HGDNPVPVSYINANIIMPEFETKCNN 320
 QY 95 VDGLAYIATQGPLPHTLLDFWLVWFGVKVILMACREIENGRCRCERYWAOEPLQT 154
 DB 321 SKPKSYIATQGCQLQNTVDFWVFOENSRVIMTTKEVERGSKCKVYWPDEYALKEY 380
 QY 155 GLPCTILIKEKWLNEDIMRLTKVTFOKES-----RSVYQLOYMSWDRGVPSSPDHM 207
 DB 381 GVMVRNVKES-AAHDYTLRELKLSKVGQALLQNTERTVQYHFTWPDHGVSPDPGV 439
 QY 208 LAMVEEARLQGS--GPEPLCVHCSAGCGRTGVLTVDYVQRLLTQMIQPPDFSLFDVVL 265
 DB 440 LDFLEEVHVKQESIVDAGPVVHCSAGIGRTGTFIVIDLIREKGVDCDDIVPKTIQ 499
 QY 266 KMRQORPAAVOTEQRYFLYHTVAQMFCSLTQ-----NASPHYQNIKENCAPLYD 315
 DB 500 MVRQSRGVMQTEAQRYFIYNAV-QHYETLQRIEIEQSKRGKHEYNIKSS---LVD 555
 QY 316 DALFLRTPOALLAIPRPPGVLRIS 341
 DB 556 QTSQDSPLP-PCPTPTPPCAEMRDS 580

RESULT 15
 A44267
 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1 - slime mold (Dictyostelium
 C:Species: Dictyostelium discoideum
 C:Date: 30-Apr-1993 #sequence_revision 08-Mar-1996 #text_change 24-Apr-1998
 C:Accession: A44267
 R:Howard, P.K.; Sefton, B.M.; Firtel, R.A.
 Cell 71, 637-647, 1992
 A>Title: Analysis of a spatially regulated phosphotyrosine phosphatase identifies tyrosin
 A:Reference number: A44267; MUID:93046662; PMID:1423620
 A:Accession: A44267
 A>Status: nucleic acid sequence not shown; not compared with conceptual translation
 A:Molecule type: mRNA; DNA
 A:Residues: 1-521 <HOW>
 A>Note: sequence extracted from NCBI backbone (NCBIP:117713)
 C:Superfamily: Dictyostelium protein-tyrosine-phosphatase, nonreceptor type 1; protein-ty
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:121-459/Domain: protein-tyrosine-phosphatase homology #status atypical <PTP>
 F:310/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:316/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.5%; Score 448; DB 1; Length 521;
 Best Local Similarity 29.0%; Pred. No. 3.9e-25;
 Matches 113; Conservative 53; Mismatches 88; Indels 136; Gaps 13;

QY 44 GVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLQEGHSDYINGNFIKRGVDSL--AY 101
 DB 109 GPSETSGDKKENTSKRYTNILPVNTRVQLKIQKESGDYINANYI---DGAYPKQF 165
 QY 102 IATQGPLPHTLLDFWLVWFGVKVILMACREIENGRCRCERYWAOEPLQGLF---- 157
 DB 166 ICTQGPLNTIADFWVMWENRCRIIVMLSRESENCRICKDRIYWPQIGQEQSIYNGN 225
 QY 158 -----CITLLIKKWLNEDIMRLTKVTFOKESRSVYQLOYMSWDRGVPSSPDH-- 206
 DB 226 EVFGTYSVELVEVLQDP--EREITNIRLITFGETRDTIQYEGWPDHNI---PDHTQ 280

Qy	207	-----MLAMVEEARLQSGPE--PLCVHCSAGCGRTGVLCTV-----DYVROLLLT	251
Db	281	PFQQLHSITNRQNIIFSSDRNVPIIVHCSAGVGRGTCTAVIMMKLDHYFKOLDAT	340
Qy	252	---QMIPP-----	256
Db	341	PIDQVDPFTHLPITEYQSDNLDLKGLGYHFKSSIYNSNGINNNNNNNNNNNNNNNNN	400
Qy	257	-----DPSLFDVVLKMRKORPAAVQTEEQY	281
Db	401	GSNTPQTEPNNEEDDDAAESTKYAIMDKYNSRIDENLFSIVLKLREQRFQGMVQOLEQY	460
Qy	282	REFLYTV-AQMF-----CSTLQNASPHYQNI	306
Db	461	LFCYXILAEIYHRLNCK-LGFSLPHVNNI	489

Search completed: August 17, 2004, 20:44:35
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:29:38 ; Search time 14 seconds
(without alignments)
1703.438 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 2424

Sequence: 1 MSRLDSARSFLERLEARGG.....NLIRGKGRDPPAEWTRV 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2424	100.0	458	1 PTNI_HUMAN	Q99952 homo sapien
2	755.5	31.2	802	1 PTNB_MOUSE	P29352 mus musculus
3	727.5	30.0	807	1 PTNB_HUMAN	Q9Y2R2 homo sapien
4	709	29.2	780	1 PTNC_HUMAN	Q05209 homo sapien
5	703	29.0	775	1 PTNC_MOUSE	P35831 mus musculus
6	485	20.0	1705	1 PTPV_MOUSE	P70289 mus musculus
7	482.5	19.9	613	1 PTN6_RAT	P81718 rattus norv
8	475.5	19.6	595	1 PTN6_MOUSE	P29351 mus musculus
9	474	19.6	1711	1 PTPV_RAT	Q64612 rattus norv
10	463	19.1	595	1 PTN6_HUMAN	P29350 homo sapien
11	462	19.1	926	1 PTN4_HUMAN	P29074 homo sapien
12	453	18.7	593	1 PTNB_CHICK	Q90687 gallus gall
13	453	18.7	593	1 PTNB_HUMAN	Q06124 homo sapien
14	451	18.6	585	1 PTNB_MOUSE	P35235 mus musculus
15	448	18.5	593	1 PTNB_RAT	P41499 rattus norv
16	448	18.5	913	1 PTN3_HUMAN	P36045 homo sapien
17	447	18.4	521	1 PTP1_DICDI	P34137 dictyosteli
18	435	17.9	1337	1 PTPJ_HUMAN	Q12913 homo sapien
19	430.5	17.8	435	1 PTN1_HUMAN	P18031 homo sapien
20	430	17.7	593	1 PTN9_HUMAN	P43378 homo sapien
21	428	17.7	1026	1 PTP1_CAEEL	P28191 caenorhabdi
22	426.5	17.6	802	1 PTPA_HUMAN	P18433 homo sapien
23	426	17.6	434	1 PTP9_DROME	Q13016 gallus gall
24	424	17.5	1301	1 PTP9_MOUSE	P35832 drosophila
25	423.5	17.5	829	1 PTNA_MOUSE	P18052 mus musculus
26	421.5	17.4	1238	1 PTPJ_MOUSE	Q64455 mus musculus
27	421.5	17.4	2316	1 PTPZ_RAT	Q62656 rattus norv
28	421.5	17.4	2485	1 PTND_HUMAN	Q12923 homo sapien
29	420	17.3	360	1 PTN7_HUMAN	P35236 homo sapien
30	419.5	17.3	1216	1 PTPO_HUMAN	Q16827 homo sapien
31	419.5	17.3	1997	1 PTPB_HUMAN	P23467 homo sapien
32	419	17.3	1442	1 PTPG_MOUSE	Q05909 mus musculus
33	419	17.3	1445	1 PTPG_HUMAN	P23470 homo sapien

34	418.5	17.3	1897	1 PTPF_HUMAN	P10586 homo sapien
35	417.5	17.2	1912	1 PTPD_HUMAN	P23468 homo sapien
36	417	17.2	2200	1 LAR_CAEEL	Q9bmn8 caenorhabdi
37	416	17.2	1454	1 PTPT_MOUSE	Q99m80 mus musculus
38	416	17.2	1463	1 PTPT_HUMAN	O14522 homo sapien
39	415.5	17.1	1463	1 PTPM_MOUSE	P28828 mus musculus
40	414.5	17.1	359	1 PTN7_RAT	P49445 rattus norv
41	414.5	17.1	1015	1 PTPX_HUMAN	Q92932 homo sapien
42	414.5	17.1	1948	1 PTNS_HUMAN	Q13332 homo sapien
43	413.5	17.1	2314	1 PTPZ_HUMAN	P23471 homo sapien
44	412.5	17.0	1013	1 PTPX_MACNE	O02695 macaca name
45	411.5	17.0	432	1 PTN1_RAT	P20417 rattus norv

ALIGNMENTS

RESULT 1

ID	PTNI_HUMAN	STANDARD;	PRT;	458 AA.
AC	Q99952;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Protein-tyrosine phosphatase, non-receptor type 18 (EC 3.1.3.48)			
DE	(brain-derived phosphatase).			
GN	PTPN18 OR BDPI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND CHARACTERIZATION.			
RC	TISSUE=Brain;			
RX	MEDLINE=97108674; PubMed=8950995;			
RA	Kim Y.W., Wang H.Y., Suess I., Lambers R., Martell K.J., Ullrich A.;			
RT	"Characterization of the PEST family protein tyrosine phosphatase			
RT	BDPI.";			
RL	Oncogene 13:2275-2279(1996).			
CC	-!- FUNCTION: Differentially dephosphorylate autophosphorylated			
CC	tyrosine kinases which are known to be overexpressed in tumor			
CC	tissues.			
CC	-!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein			
CC	tyrosine + phosphate.			
CC	-!- TISSUE SPECIFICITY: Expressed in brain, colon and several tumor-			
CC	derived cell lines.			
CC	-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.			
CC	Non-receptor class subfamily.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X79568; CAA56105.1; -			
DR	HSSP; Q66124; 2SHP; PTPN18.			
DR	Genew; HGNC:9649; PTPN18.			
DR	MIM; 606587; -			
DR	GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . . ; TAS.			
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.			
DR	InterPro; IPR000387; TYR_phosphatase.			
DR	InterPro; IPR000242; Tyr_PP			
DR	Fram; PF00102; Y_phosphatase; 1.			
DR	PRINTS; PR00700; EPTYPHPTASE.			
DR	SMART; SM00194; PTPC; 1.			
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.			
DR	PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.			
DR	PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.			
KW	Hydrolase.			
FT	DOMAIN 26 291 PROTEIN-TYROSINE PHOSPHATASE.			

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FT ACT_SITE 229 229 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY)
SQ SEQUENCE 458 AA; 50384 MW; 46BCA1E17C278B1 CRC64;

Query Match 100.0%; Score 2424; DB 1; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.7e-160;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRLDSARSFLERLEARGREGAVLAGFESDIQACSAAMKADGVCSTVAGSRPENVRKN 60
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 RYKQVLPYDQTRVLSLLOEGHSDYINGNPIRGVDSGLAYIATQGPLPHTLLDFRLVW 120
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 EFGVKVILMACREIENGRKRCRYWAOBQEPLOTGLFCITLKEKWLNEIMLRLTKVTF 180
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 QKESRSVYQLYNGWDRGVSPSSPDHMLAMVEEARLQGSQGPPLCVHCSAGCGRTGVL 240
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 TVDYRQLLTQMTIPPPDPSLFDVVLKMKRKPAAVQTEBOYRFLYHTVAQMFCTIQNAS 300
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAI PRPPGGVLRISVPGSPGHAMADTYABEQKR 360
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 361 GAPAGAGSGTGTGTGARSABEAPLYSKVTPRAQRGAHAEDARGTLPGRVADQSPAG 420
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 421 SGAYEDVAGGAQTGGLGNLRIGRPKPRDPPPAETWTV 458
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
PTN8 MOUSE STANDARD; PRT; 802 AA.
AC P29352;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DE Protein-tyrosine phosphatase, non-receptor type 8 (EC 3.1.3.48)
DE (Hematopoietic cell protein-tyrosine phosphatase 702-PBP).
GN PTN8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=92236615; PubMed=1373816;
RA Matthews R.J., Bowne D.B., Flores E., Thomas M.L.;
RT "Characterization of hematopoietic intracellular protein tyrosine
RT phosphatases: description of a phosphatase containing an SH2 domain
RT and another enriched in proline-, glutamic acid-, serine-, and
RT threonine-rich sequences."
RL Mol. Cell. Biol. 12:2396-2405(1992).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Spleen, thymus, lymph node and bone marrow.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
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CC -----
CC EMBL; M90388; AAA39994.1; -.
CC PIR; B44390; B44390.
CC PDB; 1JEG; 31-OCT-01.
CC MGI; MGI:107170; Ptpn8.
CC InterPro; IPR000387; Tyr phosphatase.
CC InterPro; IPR000242; Tyr_pp.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00700; PTPYHPHATASE.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
CC Hydrolase; 3D-structure.
CC KW DOMAIN 23 288 PROTEIN-TYROSINE PHOSPHATASE. (BY
CC FT ACT_SITE 227 227 PHOSPHOCYSTEINE INTERMEDIATE
CC SIMILARITY)
CC SQ SEQUENCE 802 AA; 89714 MW; 0F1E45339BD4613E CRC64;

Query Match 31.2%; Score 755.5; DB 1; Length 802;
Best Local Similarity 44.0%; Pred. No. 8.2e-45;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;

QY 27 AGEFSDIQACSAAMKADGVCSTVAGSRPENVRKNRYKQVLPYDQTRVLSLLOEGHSDY 86
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 25 ASEFLKXQSTKYKADKIYPTTVAQRPNKIKKRYKQILFYDHSLSVLSLTDESSY 84
QY 87 INGNIRGVDSGLAYIATQGPLPHTLLDFWLVFVGVKVLMACREIENGRKCEERYWA 146
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 85 INASIRKVGYPKAYIATQGPLSTLLDFWVNIWEYRILVIVMACFEMGKKCEERYWA 144
QY 147 EQBE--PLQTGLFCITLKEKWLNEIMLRLTKVTFQKESRSVYQLYNSWPDGRVPSPD 205
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNEIRIYQFYHKWPDHDPSSID 203
QY 206 HVLAMVEEARLQSGPPLCVHCSAGCGRTGVLCYDQYRQLLTQMTIPPPDPSLFDVVL 265
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 204 PIQLIWMRCYQEDDCVPICIHCSAGCGRTGVICAVDYTWMLLKDGIIIPKQFVFNLIQ 263
QY 266 KMKRKPAAVQTEOYRFLYHTVAQMFCTIQNASPHYQNIKENCAPLYDDALFLRTPQA 325
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 264 EMRTQRPVSLVQTRQYELVYSAVLELF-----KRHMDVISDNHLG-----RIQA 308
QY 326 LLAI PRPGGVLRISVPGS-----PGHAMAD--TYAEQKRGAPAGAGSGTGTGTG 377
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 309 QCSIEP-----QSITVEADSCPLDLPKAMRDYKTTNQHSKQGAEBESTGSSGLR 362
QY 378 ARSABE 383
Dd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dd 363 TNNABE 368

RESULT 3
PTN8 HUMAN STANDARD; PRT; 807 AA.
ID PTN8 HUMAN
AC Q9V2E2; O95063; O95064;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 22 (EC 3.1.3.48)
DE (Hematopoietic cell protein-tyrosine phosphatase 702-PBP) (Lymphoid
DE phosphatase) (Lyp).
DE PTN22 OR PTPN8.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.
RX MEDLINE=9916998; PubMed=10068674;
RA Cohen S., Dadi H., Shaoul E., Sharfe N., Roifman C.M.;
RT "Cloning and characterization of a lymphoid-specific, inducible human
RL protein tyrosine phosphatase, Lyp.";
RN Blood 93:2013-2024(1999).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Liu T., Zhang J., Fu G., Zhang Q., Ye M., Zhou J., Wu J., Shen Y.,
RA Yu M., Chen S., Mao M., Chen Z.;
RT "Human protein tyrosine phosphatase (702pep) homolog.";
RL submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Seems to act on Cbl. May play a role in regulating the
CC function of Cbl and its associated protein kinases.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=tyP1;
CC IsoId=Q9Y2R2-1; Sequence=Displayed;
CC Name=2; Synonyms=Lyp2;
CC IsoId=Q9Y2R2-2; Sequence=VSP_005134;
CC -!- TISSUE SPECIFICITY: Predominantly expressed in lymphoid tissues
CC and cells. Isoform 1 is expressed in thymocytes and both mature B
CC and T cells.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
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CC -----
DR EMBL; AF001846; AAD0904.1; -
DR EMBL; AF001847; AAD0905.1; -
DR EMBL; AF077031; AAD27764.1; -
DR HSSP; P29350; 1GWZ.
DR Genew; HGNC:9652; PTPN22.
DR MIM; 600716; -
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_Pp.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PTPPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_Ptp; 1.
KW Hydroxase; Alternative splicing.
FT DOMAIN 23 288 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 227 227 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT VARSPPLIC 685 807 ELHODRSPPPPPTERTLESFFLADECMQAQIETVSTSY
FT PDWMTNSSLKQTLTKPKSFTSKSLKILRNKKIKNSC
FT PPNKPAESVQSNSSPLNFGPANRSPKPGPNPPTWNI
FT -> GNKFSWL (in isoform 2).
FT -> FTID=VSP_005134.
FT KP -> NA (IN REF. 1).
FT V -> G (IN REF. 2).
FT G -> V (IN REF. 2).
FT I -> IV (IN REF. 1).
FT L -> P (IN REF. 2).
FT M -> W (IN REF. 2).
FT P -> S (IN REF. 2).
FT SEQUENCE 807 AA; 91704 MW; 1ABE8A89C9D9F8F CRC64;
Query Match 30.0%; Score 727.5; DB 1; Length 807;
Best Local Similarity 46.9%; Pred. No. 7.1e-43;
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;
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CC EMBL; D13380; BAA02648.1; -.
CC EMBL; M93425; AAB36529.1; -.
CC EMBL; S69184; AAB30047.2; -.
CC EMBL; JCI368; JCI368.
CC HSSP; Q06124; 2SHP.
CC GENE; HGNC:9645; PTPN12.
CC MIN; 600079; -.
CC GO; GO:0005737; C:cytoplasm; TAS.
CC GO; GO:0005625; C:soluble fraction; TAS.
CC GO; GO:0004726; F:non-membrane spanning protein tyrosine phosphatase; TAS.
CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC InterPro; IPR000387; TYR_PP.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00194; PTPc; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
CC Hydrolase; Disease mutation.
FT DOMAIN 27 291 PROTEIN-TYROSINE PHOSPHATASE. (BY
FT ACT_SITE 231 231 SIMILARITY).
FT VARIANT 61 61 K->R (in colon cancer).
FT CONFLICT 121 121 V->I (IN REF. 2).
FT CONFLICT 322 322 V->I (IN REF. 2).
FT SEQUENCE 780 AA; 88092 MW; 48F7BE5FDA8F7512 CRC64;

Query Match 29.28; Score 709; DB 1; Length 780;
Best Local Similarity 41.08; Pred. No. 1.3e-41;
Matches 144; Conservative 65; Mismatches 116; Indels 26; Gaps 7;

OY 9 RSFLERLEA-----RGGREGAVLAGESFDIQACSAAMKADGVSTVAGSRPENVRKRYK 63
DB 8 RKFTQVQAKSPDHNGEDN--FARDFMRLRLSTKYRTEKIYPTATGEKEENVKRYK 65

OY 64 DVLPTDQTRVILSLQEGHSDYINGFIRGVDGLAYIATQGPLHTLLDFWLVWVEFG 123
DB 66 DILPFDHSRVLTKLTQPSQSDYINANFIRGVGPKAYATQGPLANTVIDFWRMWEYN 125

OY 124 VKVILMACREIENGKRCERYW-AQOEPLQTGLFCITILKEKWLNEDIMRLTKVTFQK 182
DB 126 VVILVACREFENGKRCERYWPLYGSDPTTFAPFKIS-CEDSQARTDYFIRLLLEFQN 184

OY 183 ESRVYQLQNSWPDROPSPDHMLAMVEARLQSGPEPLCVHCSACGRTGLCTV 242
DB 185 ESRRLYGHYVWPDHDPVPSFSDILMDISLRKYQEHEDVPICHSACGRTGAICAI 244

OY 243 DYVRLQLLTQMI PPDFSLFVWLKQRPAAYQTEQYRFLVHTVAQPCSTLQNASPH 302
DB 245 DYTWNLLKAGKIPEFNVFNLIQEMRTQHSVAQTKEQYELVHRAIAQLPEKQLQYEH 304

OY 303 YQNIKENCAPLYDDALFLRTPQALLAI-----PRPFGVLRISVPG 344
DB 305 -----GAQKIADGVNINTEENMVYSIEPEKQSDPPPKPR--TRSLVEG 347

RESULT 5
PTNC MOUSE STANDARD; PRT; 775 AA.
AC P35831;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 12 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase, P19) (P19-PTP) (MPTP-PEST).
GN PTPN12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

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OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92272714; PubMed=1590786;
RA den Hertog J., Pals C.E., Jonk L.J., Kruijer W.;
RT "Differential expression of a novel murine non-receptor protein
RT tyrosine phosphatase during differentiation of P19 embryonal
RT carcinoma cells.";
RL Biochem. Biophys. Res. Commun. 184:1241-1249(1992).
RN (2)
RP REVISIONS TO 297-416.
RX MEDLINE=93112015; PubMed=1472029;
RA Takakawa M., Itoh F., Hinoda Y., Arimura Y., Toyota M., Sekiya M.,
RA Adachi M., Imai K., Yachi A.;
RT "Cloning and characterization of a human cDNA encoding a novel
RT putative cytoplasmic protein-tyrosine-phosphatase.";
RL Biochem. Biophys. Res. Commun. 189:1223-1230(1992).
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=BA1B/C;
RX MEDLINE=95289971; PubMed=7772023;
RA Charest A., Wagner J., Shen S.H., Tremblay M.L.;
RT "Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein
RT tyrosine phosphatase.";
RL Biochem. J. 308:425-432(1995).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
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CC EMBL; X63440; CAA45037.1; ALT_SEQ.
CC EMBL; X86781; CAA60477.1; -.
CC PIR; S55345; S55345.
CC HSSP; Q06124; 2SHP.
CC MGD; MGI:104673; Ptpn12.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00194; PTPc; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
CC Hydrolase.
KW DOMAIN 27 291 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 231 231 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT CONFLICT 296 296 K->N (IN REF. 1).
FT CONFLICT 328 332 QODSP->DETS (IN REF. 1).
FT CONFLICT 380 380 W->V (IN REF. 1).
SQ SEQUENCE 775 AA; 86992 MW; 7106D73F5014E411 CRC64;

Query Match 29.08; Score 703; DB 1; Length 775;
Best Local Similarity 25.08; Pred. No. 3.3e-41;
Matches 194; Conservative 84; Mismatches 162; Indels 336; Gaps 17;

OY 9 RSFLERLEA-----RGGREGAVLAGESFDIQACSAAMKADGVSTVAGSRPENVRKRYK 63
DB 8 RKFTQVQAKSPDHNGEDN--FARDFMRLRLSTKYRTEKIYPTATGEKEENVKRYK 65

OY 64 DVLPTDQTRVILSLQEGHSDYINGFIRGVDGLAYIATQGPLHTLLDFWLVWVEFG 123
DB 66 DILPFDHSRVLTKLTQPSQSDYINANFIRGVGPKAYATQGPLANTVIDFWRMWEYN 125

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FT CARBOHYD 982 982 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 1705 AA; 186795 MW; 2783755F15387D5B CRC64;
Query Match 20.0%; Score 485; DB 1; Length 1705;
Best Local Similarity 33.4%; Pred. No. 1e-25;
Matches 134; Conservative 52; Mismatches 163; Indels 52; Gaps 12;
QY 8 ARSFLELEARGGEGAVLAGESDIOACSAANKADGVCSTVAGSRPENVRKRYKDVLP 67
DB 1132 SHSPRQYEAKSAPAHQAFQEHFELKEVGKQ-----PRLEAPANITKRYRHHVLP 1185
QY 68 YDQTRVLSLLOEBGSHDYINGNFRIGVDSGLAYIATQGLPHITLDFWRLVWFGVKVI 127
DB 1186 YDSRVLTLQSGPHSDYINANFIPGYPHQIATQGLPKTQVDFWRLVWFGVQVHVI 1245
QY 128 LMACREIENGKRCERYWAOEQEPLQGLFCITILKE-----KWLNEIDIMLRTLVKTFQKE 183
DB 1246 IMLTVGMENGRCVLCHEWPNVNSTPVTHTHTLLAESEDEWTRREFQLQH---GAEOK 1302
QY 184 SRSYVQLQYMSWDRGVPSSPDHMLMV-----BEARRLQSGGPEPLCVHCSAGCGRTGV- 238
DB 1303 QRRYKQLQFTWPDHSPVPAPSSLLAFVELVQEVKATQKG--PILVHCSAGVGRGTGF 1360
QY 239 LCTVDYVRLQLLTQMIIPDPSLFDVVLKQRKQRAVQTEQYRFLYHVAQMFCTLQ 298
DB 1361 VALLPAVRQLEEEQVW---DVNTVYILRLHRLPMITQLSQYIFLHSLCNKILSGPSD 1416
QY 299 ASPH-----YQNIKENCA--PLYDDALFLRTPOAL-LAIAPPPGGVLSRISVPGSPGHAMA 351
DB 1417 ASDSGPVPVNFPAQACAKRANANAGFLKRYLLKQAKDETGLSPS---PDYNQNSIA 1473
QY 352 DTYAEOK-----RGAPAGAGSGTQGT 374
DB 1474 SCHSQEQLALVEESPADNMLAASLPPGPGSRDHHVLTGS 1514
RESULT 7
PTN6_RAT STANDARD; PRT; 613 AA.
AC P81718;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE (Protein-tyrosine phosphatase, non-receptor type 6 (EC 3.1.3.48))
DE (Protein-tyrosine phosphatase SHP-1).
GN PTPN6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Aoki N., Yamaguchi Aoki Y., Ullrich A.;
RT "The rat SH2-containing protein-tyrosine phosphatase SHP-1 is a
RT positive regulator of NGF-induced neuronal differentiation of PC12
RT cells";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays a key role in hematopoiesis. This PTPase activity
CC may directly link growth factor receptors and other signaling
CC proteins through protein-tyrosine phosphorylation. The SH2 regions
CC may interact with other cellular components to modulate its own
CC phosphatase activity against interacting substrates (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBUNIT: Monomer (By similarity). Binds PTPNS1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -!- SIMILARITY: Contains 2 SH2 domains.
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CC -----
DR EMBL; U77038; AAD00262.1; -;
DR HSSP; P29350; IGWZ.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00017; SH2; 2.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRODOM; PD000093; SH2; 2.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00252; SH2; 2.
DR PROSITE; PS00001; SH2; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; SH2 domain; Repeat.
FT DOMAIN 6 102 SH2 1.
FT DOMAIN 112 215 SH2 2.
FT DOMAIN 246 517 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 455 PHOSPHOCYSTEINE INTERMEDIATE.
FT ACT_SITE 455 SIMILARITY).
SQ SEQUENCE 613 AA; 69578 MW; 29364B22B8F45C87 CRC64;
Query Match 19.9%; Score 482.5; DB 1; Length 613;
Best Local Similarity 36.9%; Pred. No. 4.5e-26;
Matches 108; Conservative 52; Mismatches 104; Indels 29; Gaps 8;
QY 22 EGAVLG---EFSDIQACSAANKADGVCSTVAGSRPENVRKRYKDVLPDQTRVLSLL 78
DB 239 EDTAKAGFEWEEFSLQ---KQEAKNLHQRLEGQRPENKSKRYKNILPFDHRSVIL--- 291
QY 79 QEEGH-----SDYINGNFRIGV-----DGLAVIATQGLPHITLDFWRLVWFGVKVI 127
DB 292 --QGRDSNIPGSDYINANYNQLLGGPDENSKTVIASQGLDADVDFWQAWENTRVI 349
QY 128 LMACREIENGKRCERYWAOEQEPLQGLFCITILKEKWLNEIDIMLRTLVKTFQKE--- 184
DB 350 VMTTEVEKGNKCVYPWPEVGTQRYVGLYSVTNCKEHTAE-YKLRLTQISPLDNGDLV 408
QY 185 RSVYQLQYMSWDRGVPSSPDHMLMV-----BEARRLQSGGPE--PLCVHCSAGCGRTGV 242
DB 409 REIWHYQYLSWDFHGVPEPGVLSFLDQINQROESLPHAGFIIHVSAGIGRTGIIV 468
QY 243 DVYRQLLTQMIIPDPSLFDVVLKQRKQRAVQTEQYRFLYHVAQMFCT 295
DB 469 DMLMESVTKGLDCLDIDIKTIQNVRAQSGWVQTEAQYKFIYVAIAQFIETT 521
RESULT 8
PTN6_MOUSE STANDARD; PRT; 595 AA.
ID P29351; O35128; Q63872; Q63873; Q63874; Q921G3; Q9QVA6; Q9QVA7;
AC Q9QVA8; Q9ROV6;
DT 01-DEC-1992 (Rel. 24, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE (Protein-tyrosine phosphatase, non-receptor type 6 (EC 3.1.3.48))
DE (Protein-tyrosine phosphatase 1C) (PTP-1C) (Hematopoietic cell
DE protein-tyrosine phosphatase) (70Z-SHP) (SH-PTP1).
DE PTPN6 OR PTP1C OR HCP OR HCPH.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=DBA/2;
RA MEDLINE=92123209; PubMed=1732748;
RX Yi T., Cleveland J.L., Ihle J.N.;
RA "Protein tyrosine phosphatase containing SH2 domains:
RT characterization, preferential expression in hematopoietic cells, and
RT localization to human chromosome 12p12-p13.";
RL Mol. Cell. Biol. 12:836-846(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92236615; PubMed=1373816;
RA Matthews R.J., Bowne D.B., Flores E., Thomas M.L.;
RA "Characterization of hematopoietic intracellular protein tyrosine
RT phosphatases: description of a phosphatase containing an SH2 domain
RT and another enriched in proline-, glutamic acid-, serine-, and
RT threonine-rich sequences.";
RL Mol. Cell. Biol. 12:2396-2405(1992).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS MOTHEATEN AND VIABLE MOTHEATEN.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=93133972; PubMed=8324828;
RA Schultz L.D., Schweitzer P.A., Rajan T.V., Yi T., Ihle J.N.,
RA Matthews R.J., Thomas M.L., Beier D.R.;
RT "Mutations at the murine motheaten locus are within the hematopoietic
RT cell protein-tyrosine phosphatase (Hcph) gene.";
RL Cell 73:1445-1454(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RX MEDLINE=98112780; PubMed=9445485;
RA Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
RA Lu J., Gorrell J.H., Chinnault A.C., Belmont J.W., Miller W.,
RA Gibbs R.A.;
RT "Comparative sequence analysis of a gene-rich cluster at human
RT chromosome 12p13 and its syntenic region in mouse chromosome 6.";
RL Genome Res. 8:29-40(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SUBUNIT.
RC STRAIN=C3H; TISSUE=Adrenal Gland;
RX MEDLINE=99348302; PubMed=10419485;
RA Martin A., Teui H.W., Shulman M.J., Isenman D., Tsui F.W.;
RT "Murine SHP-1 splice variants with altered Src homology 2 (SH2)
RT domains. Implications for the SH2-mediated intramolecular regulation
RT of SHP-1.";
RL J. Biol. Chem. 274:21725-21734(1999).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=22389257; PubMed=12477932;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEvan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Ketting M.C., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,
RA Butterfield V.S.N., Kryzyski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 54-68; 128-135; 137-151; 242-252; 278-285; 293-308 AND
RP 373-382, AND PHOSPHORYLATION
RX MEDLINE=93054686; PubMed=1385421;
RA Yeung Y.-G., Berg K.L., Pixley F.J., Angeletti R.H., Stanley E.R.;
RT "Protein tyrosine phosphatase-1C is rapidly phosphorylated in tyrosine
RT in macrophages in response to colony stimulating factor-1.";
RL J. Biol. Chem. 267:23447-23450(1992).
RN [8]
RP INTERACTION WITH PTPNS1.
RX MEDLINE=98380500; PubMed=9712903;
RA Veillette A., Thibaut E., Latour S.;
RT "High expression of inhibitory receptor SHPS-1 and its association
RT with protein tyrosine phosphatase SHP-1 in macrophages.";
RL J. Biol. Chem. 273:22719-22728(1998).
RN [9]
RP FUNCTION: Plays a key role in hematopoiesis. This PTPase activity
CC may directly link growth factor receptors and other signaling
CC proteins through protein-tyrosine phosphorylation. The SH2 regions
CC may interact with other cellular components to modulate its own
CC phosphatase activity against interacting substrates.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBUNIT: Monomer. Binds PTPNS1.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=P29351-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P29351-2; Sequence=VSP_005131;
CC Name=3;
CC IsoId=P29351-3; Sequence=VSP_005132, VSP_005133;
CC -!- TISSUE SPECIFICITY: Expressed predominantly in hematopoietic
CC cells.
CC -!- PTM: Phosphorylated on tyrosine residues.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC -!- Non-receptor class subfamily.
CC -!- SIMILARITY: Contains 2 SH2 domains.
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CC or send an email to license@isb-sib.ch).
DR EMBL; M68902; AAA37796.1; -;
DR EMBL; M90389; AAA40007.1; -;
DR EMBL; S63763; -; NOT_ANNOTATED_CDS.
DR EMBL; S63764; -; NOT_ANNOTATED_CDS.
DR EMBL; S63803; -; NOT_ANNOTATED_CDS.
DR EMBL; AC002397; AAC36009.1; -;
DR EMBL; AC002397; AAC36008.1; -;
DR EMBL; U65955; AAD00152.1; -;
DR EMBL; U65952; AAD00152.1; JOINED.
DR EMBL; U65953; AAD00152.1; JOINED.
DR EMBL; U65954; AAD00152.1; JOINED.
DR EMBL; U65955; AAD00151.1; -;
DR EMBL; U65951; AAD00151.1; JOINED.
DR EMBL; U65952; AAD00151.1; JOINED.
DR EMBL; U65953; AAD00151.1; JOINED.
DR EMBL; U65954; AAD00151.1; JOINED.
DR EMBL; BC012660; AAH12660.1; -;
DR HSSP; P29350; IGWZ.
DR MGD; MGI:96055; Hcph.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR000387; TYR_phosphatase.
DR Pfam; PF00017; SH2; 2.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR PRINTS; PR00401; SH2DOMAIN.
DR ProDom; PD000093; SH2; 2.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00252; SH2; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS0055; TYR_PHOSPHATASE_FTP; 1.
DR PROSITE; PS0001; SH2; 2.

FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 431 431 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 663 663 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 737 737 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 851 851 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 882 882 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 970 970 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 982 982 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1711 AA; 187292 MW; 0F04D2D1A47A18A0 CRC64;

Query Match 19.6%; Score 474; DB 1; Length 1711;
Best Local Similarity 39.9%; Pred. No. 6e-25;
Matches 114; Conservative 35; Mismatches 111; Indels 26; Gaps 8;

Qy 10 SFLERLAARGREGAVLAGESDIQACSAWKADGVCSIVAGSRPENVRKNRYKDVLPYD 69
Db 1134 SFQSYAKSAHAHQTFQBFEELEKVGKQD-----PRLEAHPDNIIKNRPHVLPYD 1187

Qy 70 QTRVILSLOEBGHSYINGNFIQVDSLAYIATQGLPHLLDFWRLVWEFGVKVILM 129
Db 1188 HSRVRLTQCEPHSDIYNANFIPGYSHTQSIATQGLPKLTLEDFWRLVWEQVHVILM 1247

Qy 130 ACRIENGKRCERYAQOEPLQTGLFCTILKE-----KWLNEIDMLRLKLVTFQKESR 185
Db 1248 LTVGMENGRVLCEHYHPANSTPVTHGHITHLAAEPEDEWTRREFOLQ--HGTEQKQ-R 1304

Qy 186 SVYQLQYMSFDRGVSPSPDHMLAV-----EARRLQSGPEPLCVHCSAGCGRTGVLCT 241
Db 1305 RVKQLQFTTWDHVSVPAPSSLLAFVLEVQVQATQKGG--PILVHCSAGVGTGT--- 1359

Qy 242 VDYYRQLLLTQMIPP--FSLFVVLVKRKORPAAVTEQYRFLY 285
Db 1360 -FVALLRLRLQLEBEKVADVNTVYLLRLRPLMIQTLSTQYIFLH 1403

RESULT 10
PTN6 HUMAN STANDARD; PRT; 595 AA.
ID PTN6 HUMAN STANDARD; PRT; 595 AA.
AC P29350; Q969V8;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 6 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase 1C) (PTP-1C) (Hematopoietic cell
DE protein-tyrosine phosphatase) (SH-PTP1) (Protein-tyrosine phosphatase
DE SHP-1).
GN PTPN6 OR PTPIC OR HCP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=92123209; PubMed=1732748;
RA Yi T., Cleveland J.L., Ihle J.N.;
RT "Protein tyrosine phosphatase containing SH2 domains:
RT characterization, preferential expression in hematopoietic cells, and
RT localization to human chromosome 12p12-p13.";
RL Mol. Cell. Biol. 12:836-846(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RC TISSUE=Breast;
RX MEDLINE=91343005; PubMed=1652101;
RA Shen S.H., Bastien L., Posner B.I., Chretien P.;
RT "A protein-tyrosine phosphatase with sequence similarity to the SH2
RT domain of the protein-tyrosine kinases."

RL Nature 352:736-739(1991).
RN [3]
RP REVISIONS.
RA Shen S.H., Bastien L., Posner B.I., Chretien P.;
RL Nature 353:868-868(1991).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=92141214; PubMed=1736296;
RA Plutzky J., Neel B.G., Rosenberg R.D.;
RT "Isolation of a src homology 2-containing tyrosine phosphatase.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:1123-1127(1992).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX MEDLINE=95394454; PubMed=7665165;
RA Banville D., Stocco R., Shet S.H.;
RT "Human protein tyrosine phosphatase 1C (PTPN6) gene structure:
RT alternate promoter usage and exon skipping generate multiple
RT transcripts.";
RL Genomics 27:165-173(1995).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RX MEDLINE=96303695; PubMed=8723724;
RA Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E., Spanos S.,
RA Malley T., Gibbs R.A.;
RT "A gene-rich cluster between the CD4 and triosephosphate isomerase
RT genes at human chromosome 12p13.";
RL Genome Res. 6:314-326(1996).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP PHOSPHORYLATION.
RX MEDLINE=95300784; PubMed=7781604;
RA Li R.Y., Gaits F., Ragab A., Ragab-Thomas J.M.F., Chap H.;
RT "Tyrosine phosphorylation of an SH2-containing protein tyrosine
RT phosphatase is coupled to platelet thrombin receptor via a pertussis
RT toxin-sensitive heterotrimeric G-protein.";
RL EMBO J. 14:2519-2526(1995).
RN [9]
RP INTERACTION WITH LILRB1.
RX MEDLINE=97429773; PubMed=9285411;
RA Cosman D., Fanger N., Borges L., Kubin M., Chin W., Peterson L.,
RA Hsu M.-L.;
RT "A novel immunoglobulin superfamily receptor for cellular and viral
RT MHC class I molecules.";
RL Immunity 7:273-282(1997).
RN [10]
RP INTERACTION WITH LILRB2.
RX MEDLINE=99057019; PubMed=9842885;
RA Fanger N.A., Cosman D., Peterson L., Braddy S.C., Maliszewski C.R.,
RA Borges L.;
RT "The MHC class I binding proteins LIR-1 and LIR-2 inhibit Fc

receptor-mediated signaling in monocytes.";
 Eur. J. Immunol. 28:3423-3434(1998).
 [11]
 RN INTERACTION WITH PTPNS1.
 RA MEDLINE=98380500; PubMed=9712903;
 RA Veillette A., Thibautaud E., Latour S.;
 RT "High expression of inhibitory receptor SHPS-1 and its association
 RT with protein tyrosine phosphatase SHP-1 in macrophages.";
 RL J. Biol. Chem. 273:22719-22728(1998).
 [12]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 248-399.
 RX MEDLINE=9847672; PubMed=9774441;
 RA Yang J., Liang X., Niu T., Meng W., Zhao Z., Zhou G.W.;
 RT "Crystal structure of the catalytic domain of protein-tyrosine
 RT phosphatase SHP-1.";
 RL J. Biol. Chem. 273:28199-28207(1998).
 CC -!- FUNCTION: Plays a key role in hematopoiesis. This PTPase activity
 CC may directly link growth factor receptors and other signaling
 CC proteins through protein-tyrosine phosphorylation. The SH2 regions
 CC may interact with other cellular components to modulate its own
 CC phosphatase activity against interacting substrates.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- SUBUNIT: Monomer (by similarity). Binds PTPNS1, LILRB1 and LILRB2.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=Long;
 CC IsoId=P29350-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P29350-3; Sequence=VSP_007775;
 CC Name=3; Synonyms=Short;
 CC IsoId=P29350-2; Sequence=VSP_005129; VSP_005130;
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in hematopoietic
 CC cells.
 CC -!- PM: Phosphorylated on serine and tyrosine residues.
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -!- SIMILARITY: Contains 2 SH2 domains.
 CC
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 CC
 DR EMBL; M74903; AAA35963.1; .
 DR EMBL; X62055; CAA43982.1; .
 DR EMBL; M77273; AAA36610.1; .
 DR EMBL; U15528; AAA82880.1; .
 DR EMBL; U15536; AAA82880.1; JOINED.
 DR EMBL; U15535; AAA82880.1; JOINED.
 DR EMBL; U15534; AAA82880.1; JOINED.
 DR EMBL; U15533; AAA82880.1; JOINED.
 DR EMBL; U15532; AAA82880.1; JOINED.
 DR EMBL; U15531; AAA82880.1; JOINED.
 DR EMBL; U15530; AAA82880.1; JOINED.
 DR EMBL; U15529; AAA82880.1; JOINED.
 DR EMBL; U15528; AAA82879.1; .
 DR EMBL; U15537; AAA82879.1; JOINED.
 DR EMBL; U15535; AAA82879.1; JOINED.
 DR EMBL; U15534; AAA82879.1; JOINED.
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 DR EMBL; U15531; AAA82879.1; JOINED.
 DR EMBL; U15530; AAA82879.1; JOINED.
 DR EMBL; U15529; AAA82879.1; JOINED.
 DR EMBL; U47924; AAB51323.1; .
 DR EMBL; U47924; AAB51322.1; .
 DR EMBL; BC002523; AAB51322.1; .
 DR EMBL; BC007667; AAB51322.1; .

DR PIR; B42031; S20825.
 DR PDB; 1GWZ; 22-AUG-99.
 DR PDB; 1FPR; 07-MAR-01.
 DR Genew; HGNC:9658; PTPN6.
 DR MIM; 176883; .
 DR GO; GO:0016020; C:membrane; TAS.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; TAS.
 DR GO; GO:0006913; P:apoptosis; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR003595; PTPc_motif.
 DR InterPro; IPR000980; SH2_motif.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; TYR_PP.
 DR Pfam; PF00017; SH2; 2.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTYPHPHASE.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 2.
 DR SMART; SM00194; PTPC; 1.
 DR SMART; SM00404; PTPC_motif; 1.
 DR SMART; SM00252; SH2; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 Query Match 19.1%; Score 463; DB 1; Length 595;
 Best Local Similarity 32.9%; Pred. No. 9.6e-25;
 Matches 112; Conservative 56; Mismatches 110; Indels 62; Gaps 10;
 QY 22 ECAVLAG---EFSDIACSAANKADGVCSIVAGSRPENVRKRYKDLVDPYDQTRVLSLL 78
 DB 237 EDTAKAGWEEFESLQ-----KQEVKNLHQRLEGQRPENKGRYKNILPFDHSRVIL-- 289
 QY 79 QEEGH-----SDYINGNFIRGV-----DGLAYIATQGLPHLLDFWRLVWFGVKVI 127
 DB 290 ---QGRSDSNIPGSDYINANYIKNQLLGPDENAKTVIASQGLEATWDFWQMAWQENSRI 347
 QY 128 LMACREIENGKRCERYWAQEPQLTGLFCITLIKELWNEDIMLRTLVTFKES--- 184
 DB 348 VMTTEVEKGRNKCVPYFVGMQRAYGYSVTNCGEHDITE-YKLRTLVQSPDLNGDLI 406
 QY 185 RSVQLQWMSWPDGVPSSPDHMLAMVEEARLQSGGPE--PLCVHCSAGCGRTGVLCTV 242
 DB 407 REIMHYQLSWPDGVPSEPGVLSFLDQINQROESLPHAGPIIVHCSAGTGTGTIIV 466
 QY 243 DTVRQLLLTOMIPDFSLFDVVLKMKRKORPAAVQTEEQYRFLYHTVAQMFCS----- 295
 DB 467 DMLMENISTKGLDCDDIDIOKTIQWRAQRSGMVQTEAQYKFIYVAIAQFIETTKKLEVL 526
 QY 296 -----LQNA-----SPHYQNIKEN 309
 DB 527 OSQKQSEYGNITPPAMKVAHAKASRTSSKHEDVYEN 566
 RESULT 11
 PTPN4_HUMAN
 ID PTPN4_HUMAN STANDARD; PRT; 926 AA.
 AC P29074;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein tyrosine phosphatase, non-receptor type 4 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase MEG1) (PTPase-MEG1) (MEG).
 GN PTPN4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91288564; PubMed=1648233;
 RA Gu M., York J.D., Warshawsky I., Majerus P.W.;

RT "Identification, cloning, and expression of a cytosolic megakaryocyte
 RT protein-tyrosine-phosphatase with sequence homology to cytoskeletal
 RT protein 4.1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5867-5871(1991).
 RN [2].
 RC SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RC MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: May act at junctions between the membrane and the
 CC cytoskeleton.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- SIMILARITY: Contains 1 PFM domain.
 CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M68941; AAA36530.1; -;
 CC EMBL; BC010674; AAA10674.1; -;
 CC PIR; A41105; A41105.
 CC HSP; P29350; IGWZ.
 CC Genew; HGNC:9656; PTPN4.
 CC MIM; 176878; -;
 CC GO; GO:0005737; Cytoplasm; TAS.
 CC GO; GO:0004725; F:non-membrane spanning protein tyrosine phosphatase; TAS.
 CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 CC InterPro; IPR000299; Band 4.1.
 CC InterPro; IPR001478; PDZ.
 CC InterPro; IPR000387; TYR phosphatase.
 CC Pfam; PF00373; Band_41; 1.
 CC Pfam; PF00595; PDZ; 1.
 CC Pfam; PF00102; Y_phosphatase; 1.
 CC PRINTS; PR00935; BAND41.
 CC PRINTS; PR00700; PRTYPHPTASE.
 CC SMART; SM00295; B41; 1.
 CC SMART; SM00228; PDZ; 1.
 CC SMART; SM00194; PTPC; 1.
 CC PROSITE; PS00860; FERM_1; 1.
 CC PROSITE; PS00661; FERM_2; 1.
 CC PROSITE; PS00057; FERM_3; 1.
 CC PROSITE; PS01066; PDZ; 1.
 CC PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
 CC PROSITE; PS00056; TYR PHOSPHATASE 2; 1.
 CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.

KW Structural protein; Cytoskeleton; Hydrolase.
 FT DOMAIN 29 312 FERM.
 FT DOMAIN 517 589 PDZ.
 FT DOMAIN 677 926 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 852 852 PHOSPHOCYSTEINE INTERMEDIATE
 FT (BY SIMILARITY)
 SQ SEQUENCE 926 AA; 105911 MW; 4DAC6A87A675CPB0 CRC64;
 Query Match 19.1%; Score 462; DB 1; Length 926;
 Best Local Similarity 37.6%; Pred. No. 1.9e-24;
 Matches 106; Conservative 47; Mismatches 107; Indels 22; Gaps 9;
 QY 17 ARGREGAVLAGEPSDIOACSAAMKADGVCSTVAGSRPENVRKRYKDVLPYDQTRVILS 76
 Db 647 AEGLITGVILT-QFDQLYR-----KKPGMTWSCA-KLPQNIKNRYRDISPYDAFVIL- 698
 QY 77 LLOEGHSDYINGNPIRGVDSGLA-----YIATQGLPHTLDFWELVWFGVKVLMACR 132
 Db 699 ----KGNEDYINANYINMEIPSSIIQYIAQCGLPHTCTDFWQMTWEGSSVMVLT 754
 QY 133 ELENKRCERWAOEQPLQGLFCITLKEKLNEDIMLRLTKVTPQK--EGRSVYQL 190
 Db 755 QVERGRVKCHQWPEPTGSSSGYCVQVCHSEEG-NTAYIFKMTLFNQKNESEPLTQI 813
 QY 191 QYMSVPDRGVPSSPDHMLAMVVEARRLQSGPEPLCVHCSAGCGRTGLVCTVDVYVRLLL 250
 Db 814 QYIAPDHGVPDDSSDFLDFVCHVRNKRAGKEPVPVHCSAGIGRTGLITME--TAMCL 871
 QY 251 TQMIPTDFSLFVVLKMRKORPAAVQTEOYRFLYHTVAQMF 292
 Db 872 IECNQPVPL-DIVRTMRDQRAMMIQTPTSQYRHFVCEAILKVY 912
 RESULT 12
 PTNB-CHICK STANDARD; PRT; 593 AA.
 AC Q90687;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 11 (EC 3.1.3.48) (CSH-
 DE PTP2).
 GN PTPN11 OR SH-PTP2.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Aukosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Erythroblast;
 RC MEDLINE=97080506; PubMed=8921851;
 RA Park C.Y., LaMontagne K.R., Tonks N.K., Hayman M.J.;
 RT "Cloning and expression of the chicken protein tyrosine phosphatase
 RT SH-PTP2";
 RL Gene 177:93-97(1996).
 CC -!- FUNCTION: This PTPase activity may directly link growth factor
 CC receptors and other signaling proteins through protein-tyrosine
 CC phosphorylation. The SH2 regions may interact with other cellular
 CC components to modulate its own phosphatase activity against
 CC interacting substrates (By similarity). May play a positive role
 CC during the stages of erythroid cell proliferation.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in embryonic fibroblast,
 CC hematopoietic, erythroid, myeloid and lymphoid cells.
 CC -!- PTM: Phosphorylated by tyrosine-protein kinases (By similarity).
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -!- SIMILARITY: Contains 2 SH2 domains.
 CC -----
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RP ERBUTUM.
RA Tartaglia M., Mehler E.L., Goldberg R., Zampino G., Brunner H.G.,
RA Kremer H., van der Burg I., Crosby A.H., Ion A., Jeffery S.,
RA Kalidas K., Patton M.A., Kucherlapati R.S., Gelb B.D.;
RL Nat. Genet. 29:491-491(2001).
RN [11]
RP ERBUTUM.
RA Tartaglia M., Mehler E.L., Goldberg R., Zampino G., Brunner H.G.,
RA Kremer H., van der Burg I., Crosby A.H., Ion A., Jeffery S.,
RA Kalidas K., Patton M.A., Kucherlapati R.S., Gelb B.D.;
RL Nat. Genet. 30:123-123(2001).
RN [12]
RP VARIANTS NS ALA-42; ALA-60; ASN-61; GLY-72; ASP-62; CYS-63; GLY-72;
RP ILE-73; ASP-76; ARG-79; ALA-106; ASP-139; CYS-279; VAL-282; LEU-285;
RP SER-285; ASP-308; SER-308; VAL-309; LYS-501 AND VAL-504, AND VARIANT
RP NOONAN-LIKE SYNDROME SER-308.
RX MEDLINE=21987645; PubMed=11992261;
RA Tartaglia M., Kalidas K., Shaw A., Song X., Musat D.R.,
RA van der Burg I., Brunner H.G., Bertola D.R., Crosby A.H., Ion A.,
RA Kucherlapati R.S., Jeffery S., Patton M.A., Gelb B.D.;
RT "PTPN11 mutations in Noonan syndrome: molecular spectrum, genotype-
RT phenotype correlation, and phenotypic heterogeneity";
RL Am. J. Hum. Genet. 70:1555-1563(2002).
RN [13]
RP VARIANTS LEOPARD SYNDROME CYS-279 AND MET-468.
RX MEDLINE=22104852; PubMed=12058348;
RA Digilio M.C., Conti E., Sarkozy A., Mingarelli R., Dotterini T.,
RA Marino B., Pizzuti A., Dallapiccola B.;
RT "Grouping of multiple-lentiginos/LEOPARD and Noonan syndromes on the
RT PTPN11 gene";
RL Am. J. Hum. Genet. 71:389-394(2002).
RN [14]
RP VARIANTS NS ASP-62; CYS-63 AND THR-502.
RX MEDLINE=22236043; PubMed=12325025;
RA Maheshwari M., Belmont J., Fernbach S., Ho T., Molinari L., Yakub I.,
RA Yu F., Combes A., Towbin J., Craig W.J., Gibbs R.;
RT "PTPN11 mutations in Noonan syndrome type I: detection of recurrent
RT mutations in exons 3 and 13";
RL Hum. Mutat. 20:298-304(2002).
RN [15]
RP VARIANTS NS GLY-61; CYS-63; SER-72; ILE-73; SER-285 AND ASP-308.
RX MEDLINE=22151235; PubMed=12161469;
RA Kosaki K., Suzuki T., Muroya K., Hasegawa T., Sato S., Matsuo N.,
RA Kosaki R., Nagai T., Hasegawa Y., Ogata T.;
RT "PTPN11 (protein-tyrosine phosphatase, nonreceptor-type 11) mutations
RT in seven Japanese patients with Noonan syndrome";
RL J. Clin. Endocrinol. Metab. 87:3529-3533(2002).
RN [16]
RP VARIANTS JMML TYR-61; VAL-61; LYS-69; THR-72; VAL-72; ALA-76; GLY-76;
RP LYS-76; VAL-76; ALA-503 AND ARG-503, VARIANTS MYELODYSPLASTIC SYNDROME
RP VAL-60; VAL-61; LYS-69; LEU-71 AND ALA-76, VARIANTS NS ASP-62 AND
RP ILE-73, AND VARIANT ACUTE MYELOID LEUKEMIA LYS-71.
RX MEDLINE=22660528; PubMed=12717436;
RA Tartaglia M., Niemeyer C.M., Fragale A., Song X., Bueschner J.,
RA Jung A., Haehlen K., Hasle H., Licht J.D., Gelb B.D.;
RT "Somatic mutations in PTPN11 in juvenile myelomonocytic leukemia,
RT myelodysplastic syndromes and acute myeloid leukemia";
RL Nat. Genet. 34:148-150(2003).
CC -!- FUNCTION: This PTPase activity may directly link growth factor
CC receptors and other signaling proteins through protein-tyrosine
CC phosphorylation. The SH2 regions may interact with other cellular
CC components to modulate its own phosphatase activity against
CC interacting substrates.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBUNIT: Binds PTPNS1.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Widely expressed; particularly abundant in
CC heart, brain, and skeletal muscle.
CC -!- PTM: Phosphorylation of tyrosine residues at the C-terminus by
CC platelet-derived growth factor creates a binding site for the SH2
CC domain of GRB2.
CC -!- DISEASE: Defects in PTPN11 are the cause of LEOPARD syndrome

[MIM:151100], an autosomal dominant disorder allelic with Noonan
syndrome. The acronym LEOPARD stands for lentiginos,
electrocardiographic conduction abnormalities, ocular
hypertelorism, pulmonic stenosis, abnormalities of genitalia,
retardation of growth, and deafness.
-!- DISEASE: Defects in PTPN11 are a cause of Noonan syndrome (NS)
[MIM:163950]; also designated Noonan syndrome 1 (NS1). NS is an
autosomal dominant disorder characterized by dysmorphic facial
features, short stature, hypertelorism, cardiac anomalies,
deafness, motor delay, and a bleeding diathesis. It is a
genetically heterogeneous and relatively common syndrome, with an
estimated incidence of 1 in 1000-2500 live births. Mutations in
PTPN11 account for more than 50% of the cases. Rarely, NS is
associated with juvenile myelomonocytic leukemia (JMML).
-!- DISEASE: Defects in PTPN11 are a cause of Noonan-like syndrome
[MIM:163955]; also known as Noonan-like/multiple giant cell lesion
syndrome. It is an autosomal dominant disorder characterized by
Noonan features associates with giant cell lesions of bone and
soft tissue.
-!- DISEASE: Defects in PTPN11 are a cause of juvenile myelomonocytic
leukemia (JMML) [MIM:607785], a pediatric myelodysplastic syndrome
that constitutes approximately 30% of childhood cases of
myelodysplastic syndrome (MDS) and 2% of leukemia.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC -!- SIMILARITY: Contains 2 SH2 domains.
CC -----
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CC -----
DR ENBL; L08807; ; NOT ANNOTATED_CDS.
DR ENBL; X70766; CAA50045.1; -
DR ENBL; D13540; BAA02740.2; -
DR ENBL; L07527; AAA17022.1; -
DR ENBL; L03535; AAA36611.1; -
DR PIR; JN0805; JN0805.
DR PDB; 2SHF; 16-FEB-99.
DR Genew; HGNC:9644; PTPN11.
DR MIM; 176876; -.

Query Match 18.7%; Score 453; DB 1; Length 593;
Best Local Similarity 33.8%; Pred. No. 4.7e-24;
Matches 119; Conservative 53; Mismatches 126; Indels 54; Gaps 12;

Qy 1 MRSLSASRFLERLEARGREGAVLA-----GEPSDI--QACSAANKADGVCS 47
Db 212 LKQPLNTTRINAAEIESR-VRELSKLAETTDKVGQFWEEFTLQOQCECKLY-----S 264
Qy 48 TVAGSRPENVRKNRYKDVLPDQTRVILSLQEGH-----SDYINGNFI-----RG 94
Db 265 RGEQQRQENKKNRYKNILPFDHTRVL-----HDGDPNEPVSIDYINANILMEFETKCNN 320
Qy 95 VDGSLAYIATQGPLPHTLLDFWRLVWFGVKVILMACREIENGRKCRERYAQOEPLQT 154
Db 321 SKPKSYIATQGLQNTVNDFWRMVFNQENSRVIVMTTKEVERGKSKCVKYWDEYALKEY 380
Qy 155 GLFCITLKEKWLNEDIMLRITLKVTFQKE---SRSVYQLQVMSWPDGRGVSPSPDHMLAVY 211
Db 381 GWNVRNVKES-AAHDYTLRELKLSKVGCGNTERTVQVHFTWPDHGVSPDPGGVLDPL 439
Qy 212 EEARRLQGS--GPEPLCVHCSAGCGRTGLCTVDYVYRQLLLTQMTPPDFSLFDVVLKMKK 269
Db 440 EEVHHQESIMDAGPVVHCSAGIGRTGTFIVIDLIDILIREKGVDCDDVPEKTIQWRS 499
Qy 270 QRPAAVQTEQVRFYHTVAQMFCSLQ-----NASHYQNIKENCA 311
Db 500 QRSQMVTQAVRFYIMAV-QHYIETLQRIIEEOKSKRKKGHEYNTRIKYSLA 550

RESULT 14
PTNB MOUSE STANDARD; PRT; 585 AA.

AC P35235;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 11 (BC 3.1.3.48)
DE (Protein-tyrosine phosphatase SYP).
GN PTPN11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93206094; PubMed=8096088;
RA Feng G.-S., Hui C.-C., Pawson T.;
RT "SH2-containing phosphotyrosine phosphatase as a target of protein-
tyrosine kinases.";
RL Science 259:1607-1611(1993).
RN [2]
RN [3]
RP PTPNS1 BINDING.
RX MEDLINE=97215901; PubMed=9062191;
RA Kharitonov A., Chen Z., Sures I., Wang H., Schilling J.,
RA Ullrich A.;
RT "A family of proteins that inhibit signalling through tyrosine kinase
receptors.";
RL Nature 386:181-186(1997).
RN [3]
RX X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS) OF 4-103.
RX MEDLINE=94363243; PubMed=7521735;
RA Lee C.-H., Kominos D., Jacques S., Margolis B., Schlessinger J.,
RA Shoenelson S.E., Kuriyan J.;
RT "Crystal structures of peptide complexes of the amino-terminal SH2
domain of the Syp tyrosine phosphatase.";
RL Structure 2:423-438(1994).
CC -!- FUNCTION: This PTPase activity may directly link growth factor
receptors and other signaling proteins through protein-tyrosine
phosphorylation. The SH2 regions may interact with other cellular
components to modulate its own phosphatase activity against
interacting substrates.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
tyrosine + phosphate.
CC -!- SUBUNIT: Binds PTPNS1.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: Phosphorylated by tyrosine-protein kinases.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC -!- SIMILARITY: Contains 2 SH2 domains.
CC -!- SIMILARITY: Contains 2 SH2 domains.
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or send an email to license@isb-sib.ch).
CC EMBL; L08663; -; NOT_ANNOTATED_CDS.
DR PIR; A46209; A46209.
DR PDB; 1A5A; 31-AUG-94.
DR PDB; 1AYB; 31-AUG-94.
DR PDB; 1AYC; 31-AUG-94.
DR PDB; 1AYD; 31-AUG-94.
DR MGD; MGI:95511; Ptpn11.
DR GO; GO:0005515; P:protein binding; IPI.
DR GO; GO:0007409; P:axonogenesis; IMP.
DR GO; GO:0048011; P:NGF receptor signaling pathway; IMP.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR000387; TYR_PP.
DR InterPro; IPR00242; TYR_PP.

DR Pfam; PF00017; SH2; 2.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PRO0700; PRTYPHPTASE.
DR PRINTS; PRO0401; SH2DOMAIN.
DR ProDom; PD000093; SH2; 2.
DR SMART; SM00194; ETPC; 1.
DR SMART; SM0252; SH2; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE; PS00001; SH2; 2.
KW Hydrolase; SH2 domain; Repeat; Phosphorylation; 3D-structure.
FT DOMAIN 6 102
FT SH2 1.
FT DOMAIN 112 216
FT SH2 2.
FT DOMAIN 216 521
FT PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 463 463
FT PHOSPHOCYSTEINE INTERMEDIATE (BY
SIMILARITY).
FT TURN 5 6
FT STRAND 7 7
FT HELIX 13 22
FT TURN 23 23
FT TURN 26 27
FT STRAND 28 33
FT TURN 38 39
FT TURN 41 47
FT TURN 48 49
FT STRAND 50 55
FT STRAND 57 58
FT STRAND 63 64
FT STRAND 71 71
FT HELIX 74 83
FT TURN 85 86
FT STRAND 89 90
FT TURN 91 92
FT TURN 95 95
FT STRAND 100 101
FT STRAND 106 106
SQ SEQUENCE 585 AA; 66816 MW; 6CE554F929B8F72A CRC64;
Query Match 18.6%; Score 451; DB 1; Length 585;
Best Local Similarity 31.0%; Pred. No. 6.4e-24;
Matches 128; Conservative 59; Mismatches 142; Indels 84; Gaps 15;
QY 1 MRSLSARSFLERLEARGREGAVLA-----GEFSDI--QACSAAWADGVCS 47
DB 212 LKQPLNTRINAABIESR-VRELSKLAETTDKVKQGFWEFEFLQOQCKLLY-----S 264
QY 48 TVAGSRPENVRNRYKDVLPYDQTRVLSLQEGH-----SDYINGNFI-----RG 94
DB 265 RREGQENQKNRYKNILPFDHTEVVL---HDGDPNEPVS DYINANI IMPETETKNN 320
QY 95 VDGSLAYATQGLPHTLLDFWLVWBEFGVKVILMACREIENGKRCRYWAQOEPLQT 154
DB 321 SKPKSYATATQGLQNTWDFWVFNQNSRVVMTTZEVRGSKCVKYWPDEYALKEY 380
QY 155 GFCLTLIKELWNEIDIMRLTKVTFQES-----RSVYQLOVMSWPDGVPSSPDHM 207
DB 381 GVMRVNKRKES-AAHYTLRELKSKVQALQGNTERFTVWQYHFTWPDHGVSDPGGV 439
QY 208 LAMVEARRLQGS--GPEFLCVHCSAGCGRTGLVTDVYVRQLLLTQMIPDFSLFDVVL 265
DB 440 LDFLEEVHKKQESIVDAGFVVVHCSAGIGRTGTFIVIDILIDIRKGVDCDIDVPTIQ 499
QY 266 KVRKORPAVQTEEQRYLYHTVAQMPFCSTLQ-----NASPHYQNIKENCAPLYD 315
DB 500 MYRSQSGMVQTEAQRYFIYMAV-QHYLETQRIEIEEQKSKRGHEVTNFK-----YS 552
QY 316 DALFLRTQALLAIAPPPGGVLRSGTSVSPGCHAMADTYAEERKRGAPAGAGS 368
DB 553 GELGYTEIRV-----GCPGHSVSP--MDEVGGWVEGLGT 585
RESULT 15
PTNB_RAT

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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:38:19 ; Search time 43 Seconds

(without alignments)
3360.636 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 2424

Sequence: 1 MSRLDSARGFLERLEARGG.....NLIRGPKGPRDPPAEWTRV 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25:.*
1: sp_archaea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_mhc:.*
8: sp_organelle:.*
9: sp_phase:.*
10: sp_plant:.*
11: sp_rodent:.*
12: sp_virus:.*
13: sp_vertebrate:.*
14: sp_unclassified:.*
15: sp_virus:.*
16: sp_bacteriap:.*
17: sp_archeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1791.5	73.9	453	11 Q61152	Q61152 mus musculus
2	1782.5	73.5	453	11 Q922E3	Q922E3 mus musculus
3	1775.5	73.2	351	4 Q7Z637	Q7Z637 homo sapien
4	1775.5	73.2	372	4 Q8TA96	Q8TA96 homo sapien
5	1754.5	72.4	453	11 P70602	P70602 rattus norv
6	749.5	30.9	802	11 Q7TMP9	Q7TMP9 mus musculus
7	726.5	30.0	799	4 Q9P0D2	Q9P0D2 homo sapien
8	709	29.2	872	4 Q86XU4	Q86XU4 homo sapien
9	706	29.1	775	11 Q80UM4	Q80UM4 mus musculus
10	705.5	29.1	382	11 Q63745	Q63745 rattus norv
11	510.5	21.1	438	11 Q64642	Q64642 rattus norv
12	503.5	20.8	592	13 Q7SV37	Q7SV37 brachydanio
13	498.5	20.6	598	11 Q8BIW7	Q8BIW7 mus musculus
14	491.5	20.3	1118	4 Q15426	Q15426 homo sapien
15	489.5	20.2	1115	4 Q9HD43	Q9HD43 homo sapien
16	485	20.0	1705	11 Q9ERK5	Q9ERK5 mus musculus

17	474.5	19.6	524	4 Q9UK67	Q9UK67 homo sapien
18	471.5	19.5	336	13 Q9IB94	Q9IB94 potamotrygo
19	470	19.4	594	13 Q7ZW17	Q7ZW17 brachydanio
20	469	19.3	926	11 Q9WU22	Q9WU22 mus musculus
21	462	19.1	342	13 Q9IB95	Q9IB95 potamotrygo
22	452	18.6	597	11 Q64509	Q64509 mus musculus
23	449	18.5	292	4 Q8N4S3	Q8N4S3 homo sapien
24	447	18.4	694	13 Q7ZYN2	Q7ZYN2 xenopus lae
25	446.5	18.4	522	5 Q86AJ9	Q86AJ9 dictyosteli
26	445.5	18.4	589	13 Q803M6	Q803M6 brachydanio
27	444	18.3	595	13 Q92124	Q92124 xenopus lae
28	442	18.2	694	13 Q91870	Q91870 xenopus lae
29	441.5	18.2	470	5 Q9NL15	Q9NL15 branchiost
30	441	18.2	487	5 Q9NL13	Q9NL13 branchiost
31	441	18.2	597	13 Q91871	Q91871 xenopus lae
32	440	18.2	579	11 Q9UJ07	Q9UJ07 mus musculus
33	438	18.1	1998	11 Q8CIW2	Q8CIW2 mus musculus
34	437	18.0	461	13 Q7ZWI6	Q7ZWI6 brachydanio
35	433	17.9	1102	11 Q80VN7	Q80VN7 mus musculus
36	432.5	17.8	426	11 Q55082	Q55082 mus musculus
37	431.5	17.8	473	13 Q9NL05	Q9NL05 eptatretus
38	431	17.8	398	4 Q9Y406	Q9Y406 homo sapien
39	430	17.7	274	11 Q9CQW8	Q9CQW8 rattus norv
40	429	17.7	433	13 Q9PT91	Q9PT91 brachydanio
41	429	17.7	433	13 Q7SYN6	Q7SYN6 brachydanio
42	428	17.7	589	5 Q8MM81	Q8MM81 caenorhabdi
43	428	17.7	593	11 Q7TSK0	Q7TSK0 mus musculus
44	428	17.7	624	5 Q9U3N7	Q9U3N7 caenorhabdi
45	428	17.7	1056	13 Q8AV93	Q8AV93 petromyzon

ALIGNMENTS

RESULT 1

Q61152 PRELIMINARY; PRT; 453 AA.
ID Q61152
AC Q61152; Q62404;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (PTP-K1) (fetal liver phosphatase 1) (FLP1) (PTP 49) (PTP HSCF).
GN PTPN18 OR PTPK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RX MEDLINE=96329547; PubMed=8695832;
RA Cheng J., Daimaru L., Fennie C., Lasky L.A.;
RT "A novel protein tyrosine phosphatase expressed in lin(10)CD34(hi)Scs(hi) hematopoietic progenitor cells.";
RL Blood 88:1156-1167(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=97030045; PubMed=8875997;
RA Huang K., Sommers C.L., Grinberg A., Kozak C.A., Love P.E.;
RT "Cloning and characterization of PTP-K1, a novel nonreceptor protein tyrosine phosphatase highly expressed in bone marrow.";
RL Oncogene 13:1567-1573(1996).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=C57BL/6; TISSUE=FETAL LIVER;
RX MEDLINE=97131769; PubMed=8977243;
RA Dosil M., Leisman N., Lemischka I.R.;
RT "Cloning and characterization of fetal liver phosphatase 1, a nuclear protein tyrosine phosphatase isolated from hematopoietic stem cells.";
RL Blood 88:4510-4525(1996).
CC -!- FUNCTION: MAY BE INVOLVED IN GROWTH AND DIFFERENTIATION OF

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CC HEMATOPOIETIC CELLS.
CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN
CC TYROSINE + PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=FLPiA;
CC Name=FLPiA;
CC IsoId=Q61152-1; Sequence=Displayed;
CC Name=FLPiB;
CC IsoId=Q61152-2; Sequence=VSP_050405;
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BONE MARROW. ALSO
CC EXPRESSED IN KIDNEY, LUNG, OVARY, SPLEEN, THYMUS AND LYMPH NODE.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 15.5.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC EMBL; U35124; AAB82736.1; -.
CC EMBL; U49853; AAB18623.1; -.
CC EMBL; U52523; AAC52991.1; -.
CC HSP; Q6124; 2SHP.
CC MGD; MGI:108410; Ptpn18.
CC GO; GO:0005737; C:cytoplasm; IDA.
CC GO; GO:0005634; C:nucleus; IDA.
CC GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . .; IDA.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
CC K01; K01; 428
CC K01; K01; 229
CC ACT_SITE
CC FT VARSPIC 9 32
CC Missing (in isoform FLPIB).
CC /FTID=VSP_050405.
CC CONFLICT 11 11
CC F -> L (IN REF. 3).
CC CONFLICT 362 368
CC ASAGTG -> LRHRA (IN REF. 3).
CC SEQUENCE 453 AA; 50201 MW; 89AD7E73CE813650 CRC64;

Query Match 73.9%; Score 1791.5; DB 11; Length 453;
Best Local Similarity 75.6%; Pred. No. 5.9e-139;
Matches 347; Conservative 31; Mismatches 74; Indels 7; Gaps 2;

QY 1 MSRSLSARSFLERLEARGREGAVLAGEFSDIOACSAANKADGVCSVAGSRPENVRKN 60
DB 1 MSRTDLVRSFLEQLEARDYREGALAREFSDIKARSAVMSKGVCSVKAGSRIGNTKN 60

QY 61 RYKQVLPYDQTRVILSLLOEGHSDYINGNFIKRGVDSLAYIATQGPLPHTLLDFWRLW 120
DB 61 RYKQVAYDETRVILSLLOEGHSDYINGNFIKRGVDSLAYIATQGPLPHTLLDFWRLW 120

QY 121 EFGKVIILMACRETEGRKCRERYWAQOEPLQGLFCITLKEKWLNEIMLRILKVT 180
DB 121 EFGKVIILMACQETENGRCRERYWAQOEPLQGLFCITLKEKWLNEIMLRILKVT 180

QY 181 QKESRSVQLQYMSWPDGRVPSDDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVL 240
DB 181 QKESRSVHQLQYMSWPDGRVPSDDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVL 240

QY 241 TVDYVROLQLLTQMPDPFSLFDVVLKMKRQKPAQVQEEQVRFLYHTVAQMFCSLTQNAS 300
DB 241 ADVYVROLQLLTQMPDPFSLFDVVLKMKRQKPAQVQEEQVRFLYHTVAQMFCSLTQNAS 300

QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIAPPPGGVLSISVPGSGPHAMADTYAEQKR 360
DB 301 ADVYVROLQLLTQMPDPFSLFDVVLKMKRQKPAQVQEEQVRFLYHTVAQMFCSLTQNAS 360

QY 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTPRAQRCGAHAEDARG-TLPORVPADQSPA 419
DB 361 PHYQNIKENCAPLYDDALFLRTPQALLAIAPPPGGVLSISVPGSGPHAMADTYAEQKR 360

QY 361 GASAGTGPGRAPST-----DTPIYSQVAPRAQRPVAHTEDAQGITALLRRVPADQNSS 414
DB 361 GASAGTGPGRAPST-----DTPIYSQVAPRAQRPVAHTEDAQGITALLRRVPADQNSS 414

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QY 420 QSGAYEDYAGGAOTGGLGNLRIGRPGKPRDPPPAEWTRV 458
DB 415 GPDAYEEDVTDGAQTGGLGNLRIGRPGKPRDPPPAEWTRV 453

RESULT 2
Q922E3 PRELIMINARY; PRT; 453 AA.
ID Q922E3
AC Q922E3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to protein tyrosine phosphatase, non-receptor type 18.
GN PTPN18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC008512; AAH08512.1; -.
DR MGD; MGI:108410; Ptpn18.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . .; IDA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR Hydrolase; Receptor.
KW Hydroxylase; Receptor.
SQ SEQUENCE 453 AA; 50227 MW; 722FDE1FFC9F4689 CRC64;

Query Match 73.5%; Score 1782.5; DB 11; Length 453;
Best Local Similarity 75.6%; Pred. No. 3.2e-138;
Matches 347; Conservative 32; Mismatches 73; Indels 7; Gaps 2;

QY 1 MSRSLSARSFLERLEARGREGAVLAGEFSDIOACSAANKADGVCSVAGSRPENVRKN 60
DB 1 MSRTDLVRSFLEQLEARDYREGALAREFSDIKARSAVMSKGVCSVKAGSRIGNTKN 60

QY 61 RYKQVLPYDQTRVILSLLOEGHSDYINGNFIKRGVDSLAYIATQGPLPHTLLDFWRLW 120
DB 61 RYKQVAYDETRVILSLLOEGHSDYINGNFIKRGVDSLAYIATQGPLPHTLLDFWRLW 120

QY 121 EFGKVIILMACRETEGRKCRERYWAQOEPLQGLFCITLKEKWLNEIMLRILKVT 180
DB 121 EFGKVIILMACQETENGRCRERYWAQOEPLQGLFCITLKEKWLNEIMLRILKVT 180

QY 181 QKESRSVQLQYMSWPDGRVPSDDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVL 240
DB 181 QKESRSVHQLQYMSWPDGRVPSDDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVL 240

QY 241 TVDYVROLQLLTQMPDPFSLFDVVLKMKRQKPAQVQEEQVRFLYHTVAQMFCSLTQNAS 300
DB 241 ADVYVROLQLLTQMPDPFSLFDVVLKMKRQKPAQVQEEQVRFLYHTVAQMFCSLTQNAS 300

QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIAPPPGGVLSISVPGSGPHAMADTYAEQKR 360
DB 301 ADVYVROLQLLTQMPDPFSLFDVVLKMKRQKPAQVQEEQVRFLYHTVAQMFCSLTQNAS 360

QY 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTPRAQRCGAHAEDARG-TLPORVPADQSPA 419
DB 361 PHYQNIKENCAPLYDDALFLRTPQALLAIAPPPGGVLSISVPGSGPHAMADTYAEQKR 360

QY 361 GASAGTGPGRAPST-----DTPIYSQVAPRAQRPVAHTEDAQGITALLRRVPADQNSS 414
DB 361 GASAGTGPGRAPST-----DTPIYSQVAPRAQRPVAHTEDAQGITALLRRVPADQNSS 414

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RESULT 4
Q8TA96 PRELIMINARY; PRT; 372 AA.
ID Q8TA96
AC Q8TA96
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to protein tyrosine phosphatase, non-receptor type 18
DE (Brain-derived) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Lymph, and Lymphoma;
RC Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024280; AAH41562.1; -
DR EMBL; BC041562; AAH41562.1; -
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Receptor.
FT NON_TER 1
SQ SEQUENCE 372 AA; 40708 MW; 417CA80AA054CF8B CRC64;

Query Match 73.2%; Score 1775.5; DB 4; Length 372;
Best Local Similarity 76.2%; Pred. No. 9.3e-138;
Matches 349; Conservative 0; Mismatches 2; Indels 107; Gaps 1;

QY 1 MSRLDSARSFLERLEARGREGAVLAGFSDIQACSAANKADGVCSTVAGSRPENVRKN 60
DB 22 MSRLDSARSFLERLEARGREGAVLAGFSDIQACSAANKADGVCSTVAGSRPENVRKN 52
QY 61 RYKDVLPYDQTRVILSLQEGHSDYINGNFIKRGVDSGLAYATQGLPHTLLDFWRLVW 120
DB 53 ----- 52
QY 121 EFGVKVILMACREIENGRCERYWAQEPLOTGLFCITLKEKWLNEDIMRLTKVTF 180
DB 53 -----KRCERYWAQEPLOTGLFCITLKEKWLNEDIMRLTKVTF 94
QY 181 QKESRSYVOLQYMSWPDGRVSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLC 240
DB 95 QKESRSYVOLQYMSWPDGRVSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLC 154
QY 241 TVDYVRLQLLTQMIIPDFSLFDVVLKMRKQRPAAVQTEEQRYFLYHTVAQMFCSLTQNAS 300
DB 155 TVDYVRLQLLTQMIIPDFSLFDVVLKMRKQRPAAVQTEEQRYFLYHTVAQMFCSLTQNAS 214
QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIIPRPPGGVLRISVPSPGHAMADTYAEQKR 360
DB 215 PHYQNIKENCAPLYDDALFLRTPQALLAIIPRPPGGVLRISVPSPGHAMADTYAVVQKR 274

RESULT 3
Q7Z637 PRELIMINARY; PRT; 351 AA.
AC Q7Z637
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE PTPN18 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Lymph;
RC Strausberg R.;
RL MEDLINE=22388257; PubMed=12477932;
DR Strausberg R.L., Feingold S.A., Grouse L.H., Derge J.G.,
DR Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
DR Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
DR Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
DR Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
DR Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
DR Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
DR Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
DR Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
DR Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
DR Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
DR Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
DR Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
DR Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
DR Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
DR Krzywinski M.I., Skalska J., Smailus D.E., Schnerch A., Schein J.E.,
DR Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Lymph;
RC Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052800; AAH52800.1; -
DR EMBL; BC052800; AAH52800.1; -
SQ SEQUENCE 351 AA; 38317 MW; 5FE9B48C5D0667C4 CRC64;

Query Match 73.2%; Score 1775.5; DB 4; Length 351;
Best Local Similarity 76.2%; Pred. No. 8.6e-138;
Matches 349; Conservative 0; Mismatches 2; Indels 107; Gaps 1;

QY 1 MSRLDSARSFLERLEARGREGAVLAGFSDIQACSAANKADGVCSTVAGSRPENVRKN 60
DB 1 MSRLDSARSFLERLEARGREGAVLAGFSDIQACSAANKADGVCSTVAGSRPENVRKN 31
QY 61 RYKDVLPYDQTRVILSLQEGHSDYINGNFIKRGVDSGLAYATQGLPHTLLDFWRLVW 120
DB 32 ----- 31
QY 121 EFGVKVILMACREIENGRCERYWAQEPLOTGLFCITLKEKWLNEDIMRLTKVTF 180
DB 32 -----KRCERYWAQEPLOTGLFCITLKEKWLNEDIMRLTKVTF 73
QY 181 QKESRSYVOLQYMSWPDGRVSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLC 240
DB 74 QKESRSYVOLQYMSWPDGRVSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLC 133
QY 241 TVDYVRLQLLTQMIIPDFSLFDVVLKMRKQRPAAVQTEEQRYFLYHTVAQMFCSLTQNAS 300
DB 134 TVDYVRLQLLTQMIIPDFSLFDVVLKMRKQRPAAVQTEEQRYFLYHTVAQMFCSLTQNAS 193
QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIIPRPPGGVLRISVPSPGHAMADTYAEQKR 360
DB 194 PHYQNIKENCAPLYDDALFLRTPQALLAIIPRPPGGVLRISVPSPGHAMADTYAVVQKR 253

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QY 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTTRAQRPQGAHAEDARGTLPGRVPAQSPAG 420
DB 275 GAPAGAGSGTGTGTGARSAAEAPLYSKVTTRAQRPQGAHAEDARGTLPGRVPAQSPAG 334
QY 421 SGAYEDVAGGAQTGGLGNLRIGRPKGRDPPAEWTRV 458
DB 335 SGAYEDVAGGAQTGGLGNLRIGRPKGRDPPAEWTRV 372

RESULT 5
P70602
ID P70602 PRELIMINARY; PRT; 453 AA.
AC P70602;
DT 01-FEB-1997 (TREMELrel. 02, Created)
DT 01-FEB-1997 (TREMELrel. 02, Last sequence update)
DE 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Protein tyrosine phosphatase 20.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97067206; PubMed=8910608;
RA Aoki N., Yamaguchi-Aoki Y., Ullrich A.;
RT "The novel protein-tyrosine phosphatase PTP20 is a positive regulator
of PC12 cell neuronal differentiation.";
RL J. Biol. Chem. 271:29422-29426 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Aoki N., Yamaguchi-Aoki Y., Ullrich A.;
RL Submitted (SP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U69673; AAC52896.1; -.
DR HSSP; Q06124; 2SHP.
DR GO; GO:0004757; F:hydrolase activity; IEA.
DR GO; GO:0004755; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
DR KW Hydrolase.
SQ SEQUENCE 453 AA; 50106 MW; 6CCCI32206FB69AE CRC64;

Query Match 72.4%; Score 1754.5; DB 11; Length 453;
Best Local Similarity 74.5%; Pred. No. 6.5e-136;
Matches 342; Conservative 37; Mismatches 73; Indels 7; Gaps 3;

QY 1 MSRLDARSFLERAGREGAVILAGEPSDIOACSAANKADGVSTVAGSPENVRKN 60
DB 1 MSRQSLVRSFLEQAEARDHRKGAILAREFSDIKARSVAWKTGVSTVAGSQGSKKN 60

QY 61 RYKDVLPYDQTRVLSLLQEGHSYDINGNFRGVGSLAYIATQGPLHTLLDFWRLVW 120
DB 61 RYKDVWPEYDETRVLSLLQEGHDYINANFIRGTGSAQYIATQGPLHTLLDFWRLVW 120

QY 121 EFGVKVILMACRELENGKRCERYWAOEPIQTGLFCITLKEKWNEDIMRLTKVTF 180
DB 121 EFGKLVILMACOETENGKRCERYWAOEPIQTGLFCITLKEKWNEDIMRLTKVTF 180

QY 181 QKESRSYVQLQYMSWPDGRGPPSPDHEMLAMVEEARLQSGPPLCVHCSAGCGRTGVLC 240
DB 181 QKESRPVHQLQYMSWPDGHPVSSSDHLLTWVEEARCLQGLPGPLCVHCSAGCGRTGVLC 240

QY 241 TVDYVROLLLTOMTPPDSFLFDVVLKMRKORPAAVQTEBOYRLYITVAMFCSTLONAS 300
DB 241 ADVYVROLLLTQTPPNFSLFEVVLKMRKORPAAVQTEBOYRLYITVAMFCSTLONAS 300

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QY 301 PHYQNTKENCAPLYDDALFLRTPQALLAIPRPGGVLRISISVPGSPGHAMADTYAEOKR 360
DB 301 PHYQNLKENRAPICKDSSSLRTSSALPATSRPLGGVLRISISVPGPPTLPMDTYAVVQKR 360
QY 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTTRAQRPQGAHAEDARGTLPGRVPAQSPAG 419
DB 361 GA-----SGS-TGPGTRAPNSDITFIYSQVAPRIQRPVSHSTENAOGTTALGRVPADENPS 414
QY 420 GSCAYEDVAGGAQTGGLGNLRIGRPKGRDPPAEWTRV 458
DB 415 GPDAYEENVTDGAQTGGLGNLRIGRPKGRDPPAEWTRV 453

RESULT 6
Q7TMP9
ID Q7TMP9 PRELIMINARY; PRT; 802 AA.
AC Q7TMP9;
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DE 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055377; AAH55377.1; -.
KW Receptor.
SQ SEQUENCE 802 AA; 89694 MW; BB8C3AA618B28561 CRC64;

Query Match 30.9%; Score 749.5; DB 11; Length 802;
Best Local Similarity 43.7%; Pred. No. 7.3e-53;
Matches 160; Conservative 55; Mismatches 120; Indels 31; Gaps 7;

QY 27 AGEFSDIQACSAANKADGVSTVAGSPENVRKNRYKDVLPYDQTRVLSLLQEGHSY 86
DB 25 ASEFLKLRQKRTKTKKIYPTTVAQRPQIKKRYKDIILFYHSLVELSLTSDSDSS 84

QY 87 INGNFIRGVGSLAYIATQGPLHTLLDFWRLVWFGVKVILMACREINGKRCERYWA 146
DB 85 INASFIQGVYGFKAIIATQGPLSTLLDFWRMWEYRIILVIVMACMEFEGKKKCEHYWA 144

QY 147 QEQE-PIQTGLFCITLKEKWNEDIMRLTKVTFQKESRSYVQLQYMSWPDGRGPPSPD 205
DB 145 EPGETQLQGFPSISCEAEK-KKSDYKIRTLKAKFNNETRIYQFYHKNWPDHVPSSID 203

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QY 206 HMLAMVEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVYRQLLLTOMIPDPSLFDVWL 265
DB 204 PILELIWDMRCYQEDDCVPCIHCSAGCGRTGVCADVITWMLLKDGIIIPNFSVNLIQ 263
QY 266 KMRKORPAAVQTEQRYFLYHTVAQMFCSLQNASPHYQNIKENCAPLYDDALFLRTPOA 325
DB 264 EMRTQPSLVQTEQRYELVYSAVLEF-----KRMVDVISNHLG-----REIQ 308
QY 326 LLATPRPGVLRISVPGS-----GHAMAD--TYAESQKRGAPAGAGSGTCTGTGTG 377
DB 309 QCSLPE-----QSLTVEADSCPLDLPKNMRDVKTTNQHSHKQGAEBSTGGSLGRTS 362
QY 378 ARSAEE 383
DB 363 TMNAEE 368
RESULT 7
Q9P0U2 PRELIMINARY; PRT; 799 AA.
AC Q9P0U2;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Protein tyrosine phosphatase.
GN PTP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RA Huang C., Zhang C., Wu T., Peng Y., Gu Y., Zhang L., Jiang C., Li Y.,
RA Han Z., Wang Y., Chen Z., Fu G.;
RT "A novel gene expressed in human adrenal gland."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF150732; AAF67472.1; -.
DR HSBP; P29350; IGWZ.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000424; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 799 AA; 90610 MW; 93F5385016F33D0C CRC64;
Query Match 30.0%; Score 726.5; DB 4; Length 799;
Best Local Similarity 46.9%; Pred. No. 5.7e-51;
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;
QY 27 AGESFDIOACSAANKADGVCSTVAGSRPENVRKRYKDVLPYDQTRVILSLQEGHSDY 86
DB 25 ANEFLKRSQTKYKADTYPTTVAEKPKIKKRYKDIILPYDSRVLSLSITSDSSY 84
QY 87 INGNFIRGVDGSLAVIATQGPLPHTLLDFWLVWFVGVKVLMACREIENGKRCERYWA 146
DB 85 INANFIKVGYPEAVIATQGPLSTLLDFWNIWEYSVLIIVMACMEYENGKKRCERYWA 144
QY 147 QEQE-PLQTGLFCITLIKELKWNEDIMLRTLVKTFQKESRSVYQLQYMSWDRGVPSPPD 205
DB 145 EPGEMQLEFGPPSVSCEAEK-RKSDYIIRTLKVFNSERTIYQPHYKNWPDHDPVSSID 203
QY 206 HMLAMVEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVYRQLLLTOMIPDPSLFDVWL 265
DB 204 PILELIWDMRCYQEDDCVPCIHCSAGCGRTGVCADVITWMLLKDGIIIPNFSVNLIR 263

QY 266 KMRKORPAAVQTEQRYFLYHTVAQMF---CSLQNASPHYQNIKENCAP 312
DB 264 EMRTQPSLVQTEQRYELVYSAVLEFRLQMDVIRDKHSGTESQAKHCIP 313
RESULT 8
Q86XU4 PRELIMINARY; PRT; 872 AA.
AC Q86XU4;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 12 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC050008; AAH50008.1; -.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003595; PTPC_motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000424; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC_motif; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 1.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 872 AA; 97952 MW; 84621458356585D4 CRC64;
Query Match 29.2%; Score 709; DB 4; Length 872;
Best Local Similarity 40.7%; Pred. No. 1.8e-49;
Matches 143; Conservative 66; Mismatches 116; Indels 26; Gaps 7;
QY 9 RSFLERLEA-----RGREGAVLAGEFSDIQACSAANKADGVCSTVAGSRPENVRKRYK 63
DB 100 RKFQIRVQAMKSPDHNGEDN--FARDFMRLRLSKYRTEKIYPTATGKEENVKKNRYK 157
QY 64 DVLVPYDQTRVILSLQEGHSDYINGNFIRGVDGSLAVIATQGPLPHTLLDFWLVWFV 123
DB 158 DILPFDHSVSKLTLTPTSDSDYINANFIKVGYPKAYVATQGPLANTVIDFWRMIWEYN 217
QY 124 VKVILMACREIENGKRCERYW-AQEQLPQTGLFCITLIKELKWNEDIMLRTLVKTFQK 182
DB 218 VLIIVNACREFEMGRKKERYWPLYGEDPITTFAPPKIS-CEDEQARTDYFIITLLLEFQN 276
QY 183 ESRSVYQLQYMSWDRGVSPDPHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCTV 242
DB 277 ESRLLQFYHYVWPDHVDVPSFSDSLDMSLMKRYQEHEDVFCIHCSAGCGRTGAICAI 336
QY 243 DYVROLQLLTQMIPDPSLFDVVLKMRKORPAAVQTEQRYFLYHTVAQMFCSLQNASPH 302
DB 337 DYTWNLLKAGKPIEENFNENLIQEMRTQSHSAVQTEQRYELVHRAIAQLFEKQLQIYEIH 396
QY 303 YQNIKENCAPLYDDALFLRTPOALLAI-----PRPPGGVLRISVPG 344
DB 397 -----GAQKIADGVNNEINMISSIEBPCKPPKPPR---TRSLVEG 439
RESULT 9
Q80UM4 PRELIMINARY; PRT; 775 AA.
ID Q80UM4

AC Q80UM4;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to protein tyrosine phosphatase, non-receptor type 12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kertanen M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Strausberg R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC051980; AAH51980.1; -
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0004872; P:receptor activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR003595; PTPC_motif.
 DR InterPro; IPR000387; TVR_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PTRYPHPTASE.
 DR SMART; SM00194; PTPC; 1.
 DR SMART; SM00404; PTPC motif; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_Ptp; 1.
 KW Receptor.
 SQ SEQUENCE 775 AA; 86526 MW; EDIA7AS77CE4352C CRC64;
 Query Match 29.1%; Score 706; DB 11; Length 775;
 Best Local Similarity 25.1%; Pred. No. 2.7e-49;
 Matches 195; Conservative 83; Mismatches 162; Indels 336; Gaps 17;
 QY 9 RSFLERLEA-----RGREGAVLAGEFSDIQACSAANKADGVCSVAGSPENVNRKRYK 63
 DB 8 RRFQVRQAMKSPDHNEEDN--FARDFMRLRLLSTKRTKRIYPTATGEEKENVKKRYK 65
 QY 64 DVLFDYQTRVLSLLQBEHSDYINGNFIKRGVDSGLAYIATQGPLHTLDFWRLVWFEFG 123
 DB 66 DILPFDHSRVKLTKTSPQSDYINANFNGVYGPAYVATQGPLANTVIDFWMIWEYN 125
 QY 124 VKVILMACREINERKRCERYW-AQOEPEQTGLFCITLKEKWLINEDIMRLKVTFOK 182
 DB 126 VVIIVMACREFEMGRKKCKERYWLYGSDPTITFAFKISCENEQ-ARTDYFIRTLLEFQN 184
 QY 183 ESRVYQLQYMSWDRGVSPSPDHMLANVBEARRLQSGPEPLCVHCSAGCGRTGVLCTV 242

DB 185 ESRRLYQHYVNVWPHDVPSPDFSDILMTISLMRYQEHEDVFCIHCSAGCGRTGAICAI 244
 QY 243 DYVRQLLTQMIPDPFSLFDVVLKMKRKORPAAVQTEEOYRFLYHTVAQMFCSLTQ---- 297
 DB 245 DTWNLLKAGKIPDEFNFVNLICQEMRTQHSVAQVKEQYELVHRAIAQIFKQLQLYEIH 304
 QY 298 ----- 297
 DB 305 GAKIADGNEITTTGTMVSSIDSEKQDPPPKPRTSRCLVEGDAXEILQPPEHPVPPI 364
 QY 298 -----NAP----- 301
 DB 365 LTFPPSPAPPTVTWQSDRHYKPVLMASPEQHPADLNRSDYKSDADPMCKSESAIEH 424
 QY 302 -----HYQIKENCAFLYDDALFLRT--PQA 325
 DB 425 IDKLLERNLSFEIKKVLQEGPKSFDGNTLLNRGHAIKIKSASSVWD-----RTSKPQE 479
 QY 326 ILA-----IPRP-----PGGVLRSI- 340
 DB 480 LSAGALKVDDVDSQNSCADSAHSHRAAESSESSQNSHTPPRDCPLDKKGHVTVSLH 539
 QY 341 -----SVPGSPGHAMADTY-----AEQKR----- 360
 DB 540 GPNATPVDPDGDGKSPDNHSQTLKTVSSTPNSTAEEAHDLTEHNSSPLLKAPLSFTN 599
 QY 361 -----CAPAGAGSGTGTGTGA-----RSAAEAPLYSKVTPR----- 393
 DB 600 PLHSDSDSDGSGSDGAVTRNKTSISTASATVSPASSAESACTRVLPMSTARQEVAGTP 659
 QY 394 ----AORPGAHADARGTLPGRPV----- 413
 DB 660 HSGAEKDADVSESPPLPPTPTPSFVLADMPVREWHLPNQEWSEQSEGLTTSQNE 719
 QY 414 -----ADQSPAGSGAYEDVA-GGAQTGGLGNLRIGRPKGRDPPPAEW 456
 DB 720 KHDAGGIHTEASADSPPAFSOKKQITKSPAEDVDIGFGNRCGKPKGPREPSEWT 775
 RESULT 10
 Q63745 ID Q63745 PRELIMINARY; PRT; 382 AA.
 AC Q63745;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Protein tyrosine phosphatase.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=95046282; PubMed=7957881;
 RA Moriyama T., Kawanishi S., Inoue T., Imai E., Kaneko T., Xia C.,
 RA Takenaka M., Kamada T., Ueda N.;
 RT "cDNA cloning of a cytosolic protein tyrosine phosphatase (RKTP) from
 RT rat kidney."
 RL FEBS Lett. 353:305-308 (1994).
 DB EMBL; D38072; BAA07266.1; -
 DR PIR; S48748; S48748.
 DR HSSP; Q06124; 2SHP.
 DR GO; GO:0016787; P:hydrolase activity; IEA.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000387; TVR_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PTRYPHPTASE.
 DR SMART; SM00194; PTPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_Ptp; 1.


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DR PROSITE; PS00383; TYR_PHOSPHATASE 1; FALSE_NEG.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Signal.
FT CHAIN 1 25 POTENTIAL.
FT CHAIN 26 1118 PROTEIN TYROSINE PHOSPHATASE.
SQ SEQUENCE 1118 AA; 123038 MW; F73E3967ECE59F00 CRC64;

Query Match 20.3%; Score 491.5; DB 4; Length 1118;
Best Local Similarity 43.3%; Pred. No. 2e-31;
Matches 116; Conservative 36; Mismatches 91; Indels 25; Gaps 9;

QY 47 STVAGSRPENVRNRYKDVLPYDQTRVILSLLOEGHSDYINGNFIRGVDSGLAYIATQG 106
Db 837 SOWVASASENNAKRYRNVLVDWSRVPLKPIHEEPGSDYINASFMPGLMSPQEFATQG 896
QY 107 PLPHTLLDFWLVWVEFGVKVILMACRIENGRKCRERYWAOEQPLQTGLFCITL----I 162
Db 897 PLPQTGVDFWLVWVEQSSHTLVMLTNCMEAGRVKCEHYWPLDSQFCTHGLRLVTLVGEEV 956
QY 163 KEKWLNEIMLRLTKVTFQKESRSYVQLQYMSWPDGRVPSPDHMLAMVEEAR-----L 217
Db 957 MENVTVRELL--LQVEEQK-TLSVRQHYQAWPDHGVPSPPDLLAFWRLQWLQDTM 1013
QY 218 QSGPEPLCVHCSAGCGRTGVLCTVD-YVRQLLLTQMIPPPDFSLFDVVLKQRKQPAVQ 276
Db 1014 EGGPP---IVHCSAGVGRGTGLIALDLLRLQSEGLLGP-----FSFVRKVRSRPLMVQ 1066
QY 277 TEEQVRLYHTVAQMFCSLQNASPHVQ 304
Db 1067 TEAQVFLH-----QCICGS-SNSQPRFQ 1089

RESULT 15
Q9HD43
ID Q9HD43 PRELIMINARY; PRT; 1115 AA.
AC Q9HD43;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transmembrane-type protein tyrosine phosphatase H.
GN PTPRH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21328879; PubMed=11435690;
RA Marneros A.G., Wehenni H., Reichenberger E., Antonarakis S.E.,
RA Krieg T., Olsen B.R.;
RT "Gene for the human transmembrane-type protein tyrosine phosphatase H
RT (PTPRH): genomic structure, fine-mapping and its exclusion as a
RT candidate for Peutz-Jeghers syndrome."
RL Cytogenet. Cell Genet. 92:213-216(2001).
DR EMBL; AF275150; AAF91411.1;
DR EMBL; AF275131; AAF91411.1; JOINED.
DR EMBL; AF275132; AAF91411.1; JOINED.
DR EMBL; AF275133; AAF91411.1; JOINED.
DR EMBL; AF275134; AAF91411.1; JOINED.
DR EMBL; AF275135; AAF91411.1; JOINED.
DR EMBL; AF275136; AAF91411.1; JOINED.
DR EMBL; AF275137; AAF91411.1; JOINED.
DR EMBL; AF275138; AAF91411.1; JOINED.
DR EMBL; AF275139; AAF91411.1; JOINED.
DR EMBL; AF275140; AAF91411.1; JOINED.
DR EMBL; AF275141; AAF91411.1; JOINED.
DR EMBL; AF275142; AAF91411.1; JOINED.
DR EMBL; AF275143; AAF91411.1; JOINED.
DR EMBL; AF275144; AAF91411.1; JOINED.
DR EMBL; AF275145; AAF91411.1; JOINED.
DR EMBL; AF275146; AAF91411.1; JOINED.
DR EMBL; AF275147; AAF91411.1; JOINED.

Query Match 20.2%; Score 489.5; DB 4; Length 1115;
Best Local Similarity 40.8%; Pred. No. 2.9e-31;
Matches 116; Conservative 43; Mismatches 98; Indels 27; Gaps 9;

QY 47 STVAGSRPENVRNRYKDVLPYDQTRVILSLLOEGHSDYINGNFIRGVDSGLAYIATQG 106
Db 835 SOWVASASENNAKRYRNVLVDWSRVPLKPIHEEPGSDYINASFMPGLMSPQEFATQG 894
QY 107 PLPHTLLDFWLVWVEFGVKVILMACRIENGRKCRERYWAOEQPLQTGLFCITL----I 162
Db 895 PLPQTGVDFWLVWVEQSSHTLVMLTNCMEAGRVKCEHYWPLDSQFCTHGLRLVTLVGEEV 954
QY 163 KEKWLNEIMLRLTKVTFQKESRSYVQLQYMSWPDGRVPSPDHMLAMVEEAR-----L 217
Db 955 MENVTVRELL--LQVEEQK-TLSVRQHYQAWPDHGVPSPPDLLAFWRLQWLQDTM 1011
QY 218 QSGPEPLCVHCSAGCGRTGVLCTVD-YVRQLLLTQMIPPPDFSLFDVVLKQRKQPAVQ 276
Db 1012 EGGPP---IVHCSAGVGRGTGLIALDLLRLQSEGLLGP-----FSFVRKVRSRPLMVQ 1064
QY 277 TEEQVRLYHTVAQMFCSLQNASPH--YONIK---ENCAPL 313
Db 1065 TEAQVFLHQCILRFLQQAQAPAEKVEPYEDVENLIYENVAI 1108

Search completed: August 17, 2004, 20:44:08
Job time : 46 secs
```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:28:43 ; Search time 54 Seconds
(without alignments)
2396.421 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 2424

Sequence: 1 MSRLDSARSPLERLEARGG.....NLRIGRPGKPRDPAETRV 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2411	99.5	458	AAW49908	AAW49908 Human bra
2	1770.5	73.0	453	AAW37254	AAW37254 Novel non
3	1764.5	72.8	353	ADC9051	ADC9051 Human KPP
4	1754.5	72.4	453	AAW49906	AAW49906 Rat prote
5	830	34.2	155	AAW37255	AAW37255 Partial h
6	755.5	31.2	802	AAW28654	AAW28654 Murine Cy
7	727.5	30.0	807	AAW89247	AAW89247 Human PTP
8	726.5	30.0	799	AAW78623	AAW78623 Human tyr
9	710	29.3	773	ABW57374	ABW57374 Mouse isc
10	709	29.2	780	AAW67252	AAW67252 Human pro
11	709	29.2	780	ADC64343	ADC64343 FLJ20037.
12	708	29.2	692	AAW28653	AAW28653 Human Cyt
13	708	29.2	780	AAW51205	AAW51205 Human Cyt
14	708	29.2	808	AAW28652	AAW28652 Human Cyt
15	705	29.1	775	AAW67250	AAW67250 Mouse pro
16	700	28.9	780	AAW51201	AAW51201 Human PTP
17	699	28.8	780	AAW67253	AAW67253 Human mut
18	698	28.8	780	AAW51202	AAW51202 Human PTP
19	695	28.7	775	AAW67251	AAW67251 Murant mo
20	665	27.4	312	AAW78281	AAW78281 Human PTP
21	658	27.1	253	AAW59383	AAW59383 Human pro
22	529	21.8	237	ADC64297	ADC64297 Human SID
23	493.5	20.4	313	AAW78277	AAW78277 Human SAP
24	491.5	20.3	1093	ABR43689	ABR43689 Human tyr
25	491.5	20.3	1118	ABR43688	ABR43688 Human tyr

26	486.5	20.1	255	4	AAW59379	AAW59379 Human pro
27	485	20.0	1705	5	ABW52348	ABW52348 Protein r
28	474	19.6	1711	2	AAW70506	AAW70506 Osteotest
29	474	19.6	1711	5	ABW52349	ABW52349 Protein r
30	468	19.3	274	4	AAW59385	AAW59385 Protein c
31	467	19.3	595	2	AAW99312	AAW99312 Human SH-
32	464	19.1	1711	2	AAW70507	AAW70507 Mutant os
33	463.5	19.1	341	4	AAW78283	AAW78283 PTP1. 12/
34	463.5	19.1	513	2	AAW99314	AAW99314 Rat M1PTP
35	463	19.1	593	2	AAW52991	AAW52991 Human pro
36	463	19.1	595	4	AAW59233	AAW59233 SHP-1 act
37	463	19.1	595	4	AAW59216	AAW59216 SHP-1 pro
38	463	19.1	595	4	AAW59239	AAW59239 SHP-1 E74
39	463	19.1	595	4	AAW59232	AAW59232 SHP-1 act
40	463	19.1	595	4	AAW59238	AAW59238 SHP-1 D59
41	463	19.1	597	3	AAW26873	AAW26873 Human Src
42	463	19.1	597	6	ABW59695	ABW59695 Human pro
43	463	19.1	621	3	AAW52289	AAW52289 Human HCP
44	463	19.1	621	5	ABW41954	ABW41954 Human ova
45	463	19.1	824	3	AAW52288	AAW52288 Human HCP

ALIGNMENTS

RESULT 1

AAW49908
ID AAW49908 standard; protein; 458 AA.

XX AAW49908;

XX AC

XX 20-JUL-1998 (first entry)

XX Human brain derived phosphatase 1 (BDP-1).

XX Brain derived phosphatase 1; BDP-1; human; receptor;

XX protein tyrosine phosphatase; signal transduction; therapy; diagnosis.

XX Homo sapiens.

XX WO9748723-A2.

XX 24-DEC-1997.

XX 17-JUN-1997; 97WO-IB000946.

XX 17-JUN-1996; 96US-0019629P.

XX 09-AUG-1996; 96US-0023485P.

XX 13-NOV-1996; 96US-0030860P.

XX 15-NOV-1996; 96US-0030964P.

XX 19-DEC-1996; 96US-0034286P.

XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

XX Ullrich A, Kharitonov AI, Aoki N, Wang HY, Chen Z, Nayler O;

XX Kim YW;

XX WPI; 1998-120302/11.

XX N-PSDB; AAV17099.

XX New phosphatase and kinase enzyme(s) - useful in the diagnosis and

XX treatment of signal transduction disorders.

XX Claim 11; Fig 3a-d; 138pp; English.

XX This polypeptide comprises a novel human protein tyrosine phosphatase
(PTP), designated brain derived phosphatase 1 (BDP-1), that is expressed
in most tissues and cell lines at basal level, but expressed high in
epithelium origin cell lines and cancer cell lines. The amino acid
sequence was deduced from a cDNA clone (see AAV17099) isolated from a
haematopoietic MEG01 cDNA library. The invention relates to novel
proteins (see AAW49906-14) involved in cellular signal transduction and
to the nucleic acids (see AAV17097-99) coding for them, and provides

CC vectors, host cells, purified recombinant proteins, methods for
 CC identifying compounds that activate or inhibit the novel proteins, as
 CC well as methods for the diagnosis and treatment of diseases associated
 CC with the novel proteins
 XX Sequence 458 AA;
 SQ
 Query Match 99.5%; Score 2411; DB 2; Length 458;
 Best Local Similarity 99.8%; Pred. No. 1.3e-220;
 Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSRSLSARSFLERLEARGREGAVLAGEFSDIOACSAAMKADGVCSVAGSPENVRKN 60
 DB 1 MSRSLSARSFLERLEARGREGAVLAGEFSDIOACSAAMKADGVCSVAGSPENVRKN 60
 QY 61 RYKDVLPYDQTRVLSLLQEGHSDYINGNFIKRVGDSLAVIATQGPPLHTLLDFWRLVW 120
 DB 61 RYKDVLPYDQTRVLSLLQEGHSDYINGNFIKRVGDSLAVIATQGPPLHTLLDFWRLVW 120
 QY 121 EFGVKVILMACREIENGKRCERYWAQOEPLQGLFCITILKEKWLNEIMLTLLKVTFF 180
 DB 121 EFGVKVILMACREIENGKRCERYWAQOEPLQGLFCITILKEKWLNEIMLTLLKVTFF 180
 QY 181 QKESRSVYQLOVMSWPDGVPSSPDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVLG 240
 DB 181 QKESRSVYQLOVMSWPDGVPSSPDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVLG 240
 QY 301 PHYQNIKENCAPLYDDALFLRTPOALLAI PRPPGGVLSISVPGSPGHAMADTYAEQOKR 360
 DB 301 PHYQNIKENCAPLYDDALFLRTPOALLAI PRPPGGVLSISVPGSPGHAMADTYAEQOKR 360
 QY 421 SGAVEDVAGGAQTGGLGNLRIGRPGKPRDPPEWTRV 458
 DB 421 SGAVEDVAGGAQTGGLGNLRIGRPGKPRDPPEWTRV 458
 RESULT 2
 AAW37254
 ID AAW37254 standard; protein; 453 AA.
 XX
 AC AAW37254;
 DT 09-APR-1998 (first entry)
 XX
 DE Novel non-receptor tyrosine phosphatase of hematopoietic stem cells.
 KW Non-receptor protein tyrosine phosphatase; hematopoietic stem cell;
 KW PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist;
 KW tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist;
 KW stem cell differentiation.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 6..303
 FT /note= "tyrosine phosphatase domain"
 FT Active-site 37
 FT /note= "phosphorylated by protein kinases A and C; also
 FT appears to negatively regulate PTPase activity"
 FT Active-site 229
 FT /note= "active site cysteine residue"
 FT Region 312..428
 FT /note= "pro, Ser and Thr rich region"
 FT Region 430..450
 FT /note= "homologous to a nuclear localization signal found

FT on murine PTP PEP"
 XX WO9735019-A1.
 XX 25-SEP-1997.
 XX 17-MAR-1997; 97WO-US005278.
 XX 22-MAR-1996; 96US-00620526.
 XX (GETH) GENENTECH INC.
 XX Lasky LA, Cheng J;
 XX WPI; 1997-480224/44.
 XX N-PSDB; AAV03112.
 PT Haematopoietic stem cell non-receptor protein tyrosine phosphatase -
 PT useful for expansion of undifferentiated stem cells in cell culture.
 XX Claim 9; Fig 1; 66pp; English.
 XX
 CC The present sequence represents a novel murine non-receptor protein
 CC tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein
 CC is predominantly expressed in early hematopoietic stem cells (HSCs) or
 CC progenitor cells, and lacks expression in adult tissues. The protein has
 CC a N-terminal tyrosine phosphatase domain, followed by a region rich in
 CC serine, threonine and proline and a C-terminal region of about 15-25
 CC amino acids which is rich in basic amino acid residues. The protein is
 CC capable of tyrosine dephosphorylation in hematopoietic progenitor cells,
 CC and functional derivatives of such native tyrosine phosphatases. The
 CC phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or
 CC progenitor cell can be used in an assay for the identification of PTP HSC
 CC antagonists or agonists. The antagonist can be used to induce the
 CC differentiation of stem cells, such as undifferentiated malignant
 CC hematopoietic cells, e.g. leukaemia cells, which may facilitate their
 CC treatment. The PTP HSC or an agonist antibody against the PTP HSC can be
 CC used for the expansion of undifferentiated stem cells in cell culture
 CC (this allows expansion of HSC prior to autologous or heterologous bone
 CC marrow transplantation), while the agonist antibody along with a
 CC hematopoietic growth factor can be used for the expansion of
 CC undifferentiated stem cells in vivo
 XX Sequence 453 AA;
 SQ
 Query Match 73.0%; Score 1770.5; DB 2; Length 453;
 Best Local Similarity 74.7%; Pred. No. 1.4e-159;
 Matches 343; Conservative 32; Mismatches 77; Indels 7; Gaps 2;
 QY 1 MSRSLSARSFLERLEARGREGAVLAGEFSDIOACSAAMKADGVCSVAGSPENVRKN 60
 DB 1 MSRSLSARSFLERLEARGREGAVLAGEFSDIOACSAAMKADGVCSVAGSPENVRKN 60
 QY 61 RYKDVLPYDQTRVLSLLQEGHSDYINGNFIKRVGDSLAVIATQGPPLHTLLDFWRLVW 120
 DB 61 RYKDVLPYDQTRVLSLLQEGHSDYINGNFIKRVGDSLAVIATQGPPLHTLLDFWRLVW 120
 QY 121 EFGVKVILMACREIENGKRCERYWAQOEPLQGLFCITILKEKWLNEIMLTLLKVTFF 180
 DB 121 EFGVKVILMACREIENGKRCERYWAQOEPLQGLFCITILKEKWLNEIMLTLLKVTFF 180
 QY 181 QKESRSVYQLOVMSWPDGVPSSPDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVLG 240
 DB 181 QKESRSVYQLOVMSWPDGVPSSPDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVLG 240
 QY 241 TVDYVYRQLLLTQMIPEFDSFLFDVLMKRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
 DB 241 ADVYVYRQLLLTQMIPEFDSFLFDVLMKRPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
 QY 301 PHYQNIKENCAPLYDDALFLRTPOALLAI PRPPGGVLSISVPGSPGHAMADTYAEQOKR 360
 DB 301 PHYQNIKENCAPLYDDALFLRTPOALLAI PRPPGGVLSISVPGSPGHAMADTYAEQOKR 360

QY 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTPRAORPGAHAEADARGTLP-CRVPADQSPA 419
 DB 361 GASAGTGGPRAPTSI-----DPIYSQVAPRAQRPAVHTEDAQGTALRRVPADQNSS 414
 QY 420 GSGAYEDVAGGAQTGGGFLNLRIGRPKGRDPPPAEWTRV 458
 DB 415 GPDAYEEVTDGAQTGGGFLNLRIGRPKGRDPPPAEWTRV 453

RESULT 3
 ID ADC99051 standard; protein; 353 AA.

AC ADC99051;
 DT 01-JAN-2004 (first entry)
 XX Human KPP protein - SEQ ID 4.
 DE
 XX anti-HIV; anti-allergic; anti-inflammatory; antianaemic; antiparkinsonian;
 KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
 KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
 KW antidiabetic; nephrotropic; antitumor; thyromimetic; neuroprotective;
 KW osteopathic; antichronic; antiparasitic; antihelminthic; antiparasitic;
 KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
 KW virucide; protozoacide; fungicide; kinase; phosphatase; KPP;
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
 KW cancer; developmental; mental retardation; neurological;
 KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
 KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
 KW helminthic infection; transgenic; gene therapy; human; enzyme.

OS Homo sapiens.
 XX WO2003033680-A2.
 XX 24-APR-2003.
 XX 17-OCT-2002; 2002WO-US033723.
 XX 19-OCT-2001; 2001US-0345474P.
 PR 02-NOV-2001; 2001US-0343910P.
 PR 13-NOV-2001; 2001US-0333098P.
 PR 16-NOV-2001; 2001US-0332424P.
 PR 30-NOV-2001; 2001US-0334288P.

(INCY-) INCYTE GENOMICS INC.
 XX Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
 PI Emerling EM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
 PI Gururajan K, Haralia Aza, Khan FA, Lal FG, Lee EA, Lee SY;
 PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
 PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
 PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
 PI Zebarjadian Y;
 XX WPI: 2003-403214/38.
 DR N-PSDB; ADC99103.
 XX New human kinases and phosphatases and polynucleotides, useful for
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
 PT cancer or hepatitis.

XX Claim 1; SEQ ID NO 4; 424pp; English.
 XX The invention relates to a novel isolated polypeptide which is a human
 CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
 CC agonists and antagonists are useful for diagnosing, treating or
 CC preventing cell proliferative disorders such as atherosclerosis,
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
 CC retardation, neurological disorders including Alzheimer's disease and
 CC Parkinson's disease, autoimmune and inflammatory disorders such as

CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the
 CC polynucleotides encoding KPP may be useful for creating transgenic
 CC animals to model human disease, as well as during gene therapy
 CC procedures. The current sequence is that of the human KPP protein of the
 CC invention.
 XX
 SQ Sequence 353 AA;

Query Match 72.8%; Score 1764.5; DB 7; Length 353;
 Best Local Similarity 75.9%; Pred. No. 3.7e-159;
 Matches 349; Conservative 0; Mismatches 2; Indels 109; Gaps 2;
 QY 1 MSRLSDARSFLERLEARGREGAVLAGFSDIQAASAAWKADGVCSVAGSRPENVRKN 60
 DB 1 MSRLSDARSFLERLEARGREGAVLAGFSDIQAASAAWKADGVCSVAGSRPENVRKN 31

QY 61 RYKDVLPYDQTRVILSLLOEBSHSDYINGNFIRGVDSLAYIATOGPLPHLLDFWRLVW 120
 DB 32 ----- 31
 QY 121 EFGVKVILMACREIENGKRCERYWAQEPLOTGLFCITLIKELKWLNEIDIMRLTKVTF 180
 DB 32 -----KRCERYWAQEPLOTGLFCITLIKELKWLNEIDIMRLTKVTF 73
 QY 181 QKESRVYQLYMSWPDGVPSSPDHMLAMVBEARLQSGPEPLCVHCSACCGRTGVLJC 240
 DB 74 QKESRVYQLYMSWPDGVPSSPDHMLAMVBEARLQSGPEPLCVHCSACCGRTGVLJC 133
 QY 241 TVDYVRQLLTQMIPPDFSLFDVWLKQKORAAVQTEBOYRFLYHTVAQMFCSLTQNAS 300
 DB 134 TVDYVRQLLTQMIPPDFSLFDVWLKQKORAAVQTEBOYRFLYHTVAQMFCSLTQNAS 193
 QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPFGVLRISIVPGSPGHAMADTYAEQKR 360
 DB 194 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPFGVLRISIVPGSPGHAMADTYAEQKR 253
 QY 361 GAPAGAGSGTQ--TGTCGARSAAEAPLYSKVTPRAORPGAHAEADARGTLPGRVPADQSP 418
 DB 254 GAPAGAGSGTQGTGTGTGARSAAEAPLYSKVTPRAORPGAHAEADARGTLPGRVPADQSP 313
 QY 419 AGSGAYEDVAGGAQTGGGFLNLRIGRPKGRDPPPAEWTRV 458
 DB 314 AGSGAYEDVAGGAQTGGGFLNLRIGRPKGRDPPPAEWTRV 353

RESULT 4
 AAM49906
 ID AAM49906 standard; protein; 453 AA.
 AC AAM49906;
 XX 20-JUL-1998 (first entry)
 DE Rat protein tyrosine phosphatase PRP20.
 KW Protein tyrosine phosphatase; PTP20; rat; signal transduction;
 KW cell differentiation; cancer; neural injury; therapy.

XX Rattus sp.
 XX OS
 XX WO9748723-A2.
 XX 24-DEC-1997.
 XX 17-JUN-1997; 97WO-IB000946.
 XX 17-JUN-1996; 96US-0019629P.
 PR 09-AUG-1996; 96US-0023485P.
 PR 13-NOV-1996; 96US-0030860P.
 PR 15-NOV-1996; 96US-0030964P.
 PR 19-DEC-1996; 96US-0034286P.

AA028654	standard; protein; 802 AA.
AA028654	(first entry)
01-OCT-1999	
Murine Cytoplasmic phosphatase, Z70PEP protein.	
Lymphoid Protein Tyrosine Phosphatase; Lyp protein; lymphoid cell; intracellular tyrosine phosphatase; PTPase; lymphocyte; murine; protein tyrosine kinase; PTKs; immunosuppressant; PEST sequence; T cell antigen receptor signalling; autoimmune disease; transplant; cytokine receptor signalling.	
Mus sp.	
Key	Location/Qualifiers
Domain	27..288
	/label= PTPase domain
	/note= "Catalytic protein tyrosine phosphatase domain"
Binding-site	613..621
	/label= SH3 binding site
	/note= "Proline rich sequence"
Binding-site	689..695
	/label= SH3 binding site
	/note= "Proline rich sequence"
Binding-site	790..798
	/label= SH3 binding site
	/note= "Proline rich sequence"
WO9336548-A1.	
22-JUL-1999.	
18-JAN-1999;	99WO-CA000038.
16-JAN-1998;	98CA-02220853.
(HSCR-) HSC RES & DEV LP.	
Roifman CM;	
WPI; 1999-444404/37.	
New nucleic acid encoding intracellular tyrosine phosphatase and related proteins, used to modulate signaling through T cells, particularly as immunosuppressant.	
Disclosure; Page 63-64; 105pp; English.	
The present protein sequence is that of the murine phosphatase, Z70PEP that has a single catalytic domain. The non-catalytic portion of the phosphatase contains unique sequences, including five PEST sequences rich in Pro, Glu or Asp, Ser and Thr. Z70PEP shares about 70% sequence identity with the human cytoplasmic phosphatase Lyp1. Lyp proteins are important for regulation of T cell antigen and cytokine receptor signalling and for early and late stages of T cell differentiation. Z70PEP has immunosuppressive activity. Compounds that increase expression of Lyp protein can be used as immunosuppressive agents to reduce or prevent T cell activation or proliferation, to control thymocyte differentiation, to treat autoimmune diseases and transplant situations	
Sequence 802 AA;	
Query Match	31.2%; Score 755.5; DB 2; Length 802;
Best Local Similarity	44.0%; Pred. No. 1.8e-62;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;	
27 AGFSDIQCSAAWKADGVCSTVAGSRDENVRKNRYKDLVYDQTRVLSLLQESGSDY 86	
25 ASBFLKRGQSTYKADKIYPTTVAQRPNKRNRYKDLVYDHSLSVLSLTSDESDSY 84	

QY	87	INGNEIRGVGDSGLAYIATQGGPLPHTLLDFWELVWFGVKVILMACREIENGKRCERYWA	146
DB	85	INASFIKGVYGPKAVIATQGPLSTLLDFWRMIWEYRILVIWACMEPEMGKKERYWA	144
QY	147	QSOE-PLQTGLFCITLKEKWLNEIMLRTIKVTFQKESRSVYQLOYMSWEDRGVPSPD	205
DB	145	BFGETQLQGFPSISCEAEK-KSDYKIRTLKAKFNENETRIIYQHYKNWPDHVPSSID	203
QY	206	HMLAWVEARRLQSGPEPLCVHCSAGCGRTGVLCTVDYVROLILTQMIPPDFSFLFVVL	265
DB	204	PIQLIWNRCYQEDDCVPICHCAGCGRTGVCADVTWMLLKDGIIIPKNFSVENLIQ	263
QY	266	KVRKQSPAAVQTEQYRFLYHTVAQMFSTLQNASPHYQNIKENCAPLYDDDLFLRTQA	325
DB	264	EMRTQPSLVQTQEQVELYSVAVLEF-----KRHMDVISDNHLG-----REIQA	308
QY	326	LLAIAPPPGGVLSISVPGS-----PGHAMAD--TYAEQKRGAPAGAGSGTGTGTG	377
DB	309	QCSIEP-----QSLTVEADSCPLDLPKNMDDVKTTHQHSKQGAESAESTGSSSLGR	362
QY	378	ARSAEE 383	
DB	363	TWNAEE 368	
RESULT 7			
AAW89247			
ID	AAW89247	standard; protein; 807 AA.	
XX	AAW89247;		
AC	AAW89247;		
DT	10-MAR-1999	(first entry)	
DE	Human PTP04.		
KW	PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease.		
OS	Homo sapiens.		
XX	WO9849317-A2.		
PD	05-NOV-1998.		
XX	27-APR-1998;	98WO-US008439.	
PR	28-APR-1997;	97US-0044428P.	
PR	20-MAY-1997;	97US-0047222P.	
PR	11-JUN-1997;	97US-0049477P.	
PR	11-JUN-1997;	97US-0049756P.	
PR	18-JUN-1997;	97US-0049914P.	
PR	23-OCT-1997;	97US-0063595P.	
PA	(SUGE-) SUGEN INC.		
XX	Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;		
PI	Courtheige SA, App H, Hui TH;		
XX	WPI; 1999-009434/01.		
DR	N-PSDB; AAV81742.		
XX	New nucleic acid encoding specific protein tyrosine phosphatases - useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease.		
PT	Claim 2; Page 151-153; 193pp; English.		
XX	The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence represents human PTP04. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify		

CC substances that modulate their activity (i.e. agonists and antagonists, including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences. CC to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the proteins

XX Sequence 807 AA;

Query Match 30.0%; Score 727.5; DB 2; Length 807;
Best Local Similarity 46.9%; Pred. No. 8.6e-60;
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;

QY 27 AGEFSDIOACSAWADGVCSTVAGSRPENVRKRYKDVLPYDQTRVILSLQEGHSDY 86
DB 25 ANEFILKQSTYKADKTYPTTVAEKPNKIKQRIKDIPLYDSRVLSLITSEDSY 84

QY 87 INGNFIRGVDGLAYIATQGPLHTLLDFWLVWFGVKVILMACREIENGKRCERYWA 146
DB 85 INANFIKGVGPEAYIATQGPLSTLLDFWMIWEYSVLLIIVMACMEYEMGKKCERYWA 144

QY 147 QOE-PLQTGLFCITLIEKWLNEIMLTAKVTQKESRSVYQLYMWPDRGVPSPD 205
DB 145 EPGEMOLEFGPFSVCEAEK-RKSDYIIRTLKVFNSSETRIYQHYKNWPDHVPSSID 203

QY 206 HMLAMVEEARLQGGPPLCVHCSAGCGRTGVLCTVDYVRLQLLTOMIPDFSLFDVWL 265
DB 204 PILELIWVRCQEDDSVPICHCAGCGRTGVCICAIDYTWMLKXGDIIPENFVSFLIR 263

QY 266 KMKQRPAAVQTEQRYFLYHTVAQMF---CSTLONASPHYQNIKENCAP 312
DB 264 EMRTQPSLVQTEQYELVYNAVLELFRQMDVIRDKHSGTESQAKHCIP 313

RESULT 8

AAAG78623
ID AAG78623 standard; protein; 799 AA.

AC AAG78623;

DT 04-DEC-2001 (first entry)

DE Human tyrosine phosphatase.

KW Human; tyrosine phosphatase; hPTP.

OS Homo sapiens.

PN CN1302899-A.

PD 11-JUL-2001.

PF 29-OCT-1999; 99CN-00119935.

PR 29-OCT-1999; 99CN-00119935.

PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.

PI Ren S, Wu T, Qian B;

DR WPI; 2001-550591/62.

DR N-PSDB; AAH79342.

PT Human protein tyrosine phosphatase and its coding sequence.

PS Claim 4; Page 12-13 (Disclosure); 29pp; Chinese.

CC The present invention provides the protein and coding sequences of human CC tyrosine phosphatase hPTP. The protein is expressed in human normal CC suprarenal tissue. The present sequence is the protein of the invention

XX Sequence 799 AA;

Query Match 30.0%; Score 726.5; DB 4; Length 799;
Best Local Similarity 46.9%; Pred. No. 1.1e-59;
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;

QY 27 AGEFSDIOACSAWADGVCSTVAGSRPENVRKRYKDVLPYDQTRVILSLQEGHSDY 86
DB 25 ANEFILKQSTYKADKTYPTTVAEKPNKIKQRIKDIPLYDSRVLSLITSEDSY 84

QY 87 INGNFIRGVDGLAYIATQGPLHTLLDFWLVWFGVKVILMACREIENGKRCERYWA 146
DB 85 INANFIKGVGPEAYIATQGPLSTLLDFWMIWEYSVLLIIVMACMEYEMGKKCERYWA 144

QY 147 QOE-PLQTGLFCITLIEKWLNEIMLTAKVTQKESRSVYQLYMWPDRGVPSPD 205
DB 145 EPGEMOLEFGPFSVCEAEK-RKSDYIIRTLKVFNSSETRIYQHYKNWPDHVPSSID 203

QY 206 HMLAMVEEARLQGGPPLCVHCSAGCGRTGVLCTVDYVRLQLLTOMIPDFSLFDVWL 265
DB 204 PILELIWVRCQEDDSVPICHCAGCGRTGVCICAIDYTWMLKXGDIIPENFVSFLIR 263

QY 266 KMKQRPAAVQTEQRYFLYHTVAQMF---CSTLONASPHYQNIKENCAP 312
DB 264 EMRTQPSLVQTEQYELVYNAVLELFRQMDVIRDKHSGTESQAKHCIP 313

RESULT 9

ABB57374
ID ABB57374 standard; protein; 773 AA.

AC ABB57374;

DT 07-MAR-2002 (first entry)

DE Mouse ischaemic condition related protein sequence SEQ ID NO:1064.

KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

KW vasospastic ischaemia; ischaemic condition; ischaemic disease.

OS Mus musculus.

PN WO200188188-A2.

PD 22-NOV-2001.

PF 18-MAY-2001; 2001WO-JP004192.

PR 18-MAY-2000; 2000JP-00145977.

PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

DR WPI; 2002-034733/04.

DR N-PSDB; ABI99910.

PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring PT expression levels of particular genes defined in the specification or by PT determining the expression profile of a gene group comprising these genes.

PS Claim 2; Page 2685-2689; 2690pp; English.

CC The present invention describes a method for examining ischaemic CC conditions, comprising measuring the expression levels of particular CC genes (I) in a test sample or determining the expression profile of a CC gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive


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Query Match          29.2%; Score 709; DB 3; Length 780;
Best Local Similarity 40.7%; Pred. No. 4.7e-58;
Matches 143; Conservative 66; Mismatches 116; Indels 26; Gaps 7;

QY 9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAMKADGVCSTVAGSRPENVRKNRYK 63
DB 8 RKFIQVQAMKSPDHNGEDN--FARDFMELRLSTKYRTEKIYPTATGKEENVKKNRYK 65

QY 64 DVLPTDQTRVILSLQEEHSDYINGNTRGVDSGLAYIATQGLPHTLLDFWRLVWFEFG 123
DB 66 DILPFDHRSVKUTLTPSQSDSYINANFIKGYGPKAYVATQGPLANTVIDFWRMWYFN 125

QY 124 VKVILMACREIENGRRKRCERYW-AQEQPLOTGLFCITLKEKWLNEIDIMLRTLVTFQK 182
DB 126 VVIIVMACREFEMGRKKERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIRTLLEFQN 184

QY 183 ESRVYQLOQYMSWPDGVPSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCV 242
DB 185 ESRRLYQHYVNWPDHVPSSFDSDILDMISLMRKYQEHEDVFCICHSAGCGRTGAICAI 244

QY 243 DYVRQLLTQMIPPDFSLFDVVLKMKRKPAAVOTEQRYFLYHTVAMFCSTLQNASPH 302
DB 245 DYTNNLLKAGKIPBEFNVFNLIQENRTQHSASVOTKEQYELVHRAIAQLFEKQLQLYEIH 304

QY 303 YONIKENCAPLYDDALFRTPOALLAI-----PRPPGVLRISIVPG 344
DB 305 -----GAQKIADGVNEINTENMISSIEPEKQDSPPPKPPR--TRSCLVEG 347

RESULT 11
ADC64343
ID ADC64343 standard; protein; 780 AA.
AC ADC64343;
XX
XX
XX 18-DEC-2003 (first entry)
XX FLJ20037.
XX Hepatotropic; vaccine; protein-protein interaction;
XX Transforming Growth Factor beta; TGF beta; hepatitis;
XX Selected Interacting Domain; SID.
XX Unidentified.
XX OS
XX WO2003045990-A2.
XX
XX 05-JUN-2003.
XX
XX 26-NOV-2002; 2002WO-EP013866.
XX
XX 26-NOV-2001; 2001US-0333348P.
XX 31-MAY-2002; 2002US-0384537P.
XX 30-OCT-2002; 2002US-0422471P.
XX
XX (HYBR-) HYBRIGENICS.
XX
XX Legrain P, Gauthier J, Colland F, Jacq X;
XX
XX WPI; 2003-505185/47.
XX N-FSDB; ADC64342.
XX
XX New complex between two interacting proteins, useful for screening
XX molecules that inhibit transforming growth factor beta (TGF beta) or TGF
XX beta super-family of cytokines pathway for diagnosing or treating TGF
XX beta diseases or disorders.
XX
XX Example 16; SEQ ID NO 127; 148pp; English.
XX
XX The present invention relates to protein-protein interactions and
XX complexes involved in Transforming Growth Factor (TGF) beta disorders
XX and/or diseases. The complex between two interacting proteins is useful
XX for screening molecules that inhibit TGF beta for diagnosing or treating

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CC diseases or disorders involving TGF beta e.g., hepatitis. To illustrate
CC the invention, Selected Interacting Domains (SID) of proteins and their
CC coding sequences were isolated (ADC64343-ADC64318). The present sequence
CC was used to illustrate the invention.
XX
SQ Sequence 780 AA;

Query Match          29.2%; Score 709; DB 7; Length 780;
Best Local Similarity 40.7%; Pred. No. 4.7e-58;
Matches 143; Conservative 66; Mismatches 116; Indels 26; Gaps 7;

QY 9 RSFLERLEA-----RGGREGAVLAGEFSDIQACSAAMKADGVCSTVAGSRPENVRKNRYK 63
DB 8 RKFIQVQAMKSPDHNGEDN--FARDFMELRLSTKYRTEKIYPTATGKEENVKKNRYK 65

QY 64 DVLPTDQTRVILSLQEEHSDYINGNTRGVDSGLAYIATQGLPHTLLDFWRLVWFEFG 123
DB 66 DILPFDHRSVKUTLTPSQSDSYINANFIKGYGPKAYVATQGPLANTVIDFWRMWYFN 125

QY 124 VKVILMACREIENGRRKRCERYW-AQEQPLOTGLFCITLKEKWLNEIDIMLRTLVTFQK 182
DB 126 VVIIVMACREFEMGRKKERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIRTLLEFQN 184

QY 183 ESRVYQLOQYMSWPDGVPSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCV 242
DB 185 ESRRLYQHYVNWPDHVPSSFDSDILDMISLMRKYQEHEDVFCICHSAGCGRTGAICAI 244

QY 243 DYVRQLLTQMIPPDFSLFDVVLKMKRKPAAVOTEQRYFLYHTVAMFCSTLQNASPH 302
DB 245 DYTNNLLKAGKIPBEFNVFNLIQENRTQHSASVOTKEQYELVHRAIAQLFEKQLQLYEIH 304

QY 303 YONIKENCAPLYDDALFRTPOALLAI-----PRPPGVLRISIVPG 344
DB 305 -----GAQKIADGVNEINTENMISSIEPEKQDSPPPKPPR--TRSCLVEG 347

RESULT 12
AAY28653
ID AAY28653 standard; protein; 692 AA.
XX
XX AAY28653;
XX
XX 01-OCT-1999 (first entry)
XX
XX Human Cytoplasmic phosphatase, Lyp2 protein.
XX
XX Lymphoid Protein Tyrosine Phosphatase; Lyp protein; immunosuppressant;
XX intracellular tyrosine phosphatase; PTPase; fetal liver; transplant;
XX resting lymphoid cell; protein tyrosine kinase; PTKs; lymphocyte;
XX T cell antigen receptor signalling; cytokine receptor signalling;
XX autoimmune disease; intronic sequence; alternative mRNA splicing.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 27..289
XX /label= PTPase domain
XX /note= "Single catalytic protein tyrosine phosphatase
XX domain"
XX Domain 469..472
XX /label= NXXY motif
XX /note= "Unique sequence recognised by phosphotyrosine
XX binding (PTB) domain"
XX Binding-site 615..623
XX /label= SH3 binding site
XX /note= "Proline rich sequence"
XX
XX WO9936548-A1.
XX
XX 22-JUL-1999.
XX
XX 18-JAN-1999; 99WO-CA000038.
XX

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PR 16-JAN-1998; 98CA-02220853.
 XX (HSCR-) HSC RES & DEV LP.
 XX Roifman CM;
 XX WPI; 1999-444404/37.
 DR N-PSDB; AAX90696.
 XX
 PT New nucleic acid encoding intracellular tyrosine phosphatase and related
 PT proteins, used to modulate signaling through T cells, particularly as
 PT immunosuppressant.
 XX
 PS Claim 4b; Page 55; 105pp; English.
 XX
 CC The present protein sequence is that of the cytoplasmic, lymphoid protein
 CC Tyrosine phosphatase, Lyp2 protein that has a single catalytic domain.
 CC The non-catalytic portion of the phosphatase contains unique sequences,
 CC including a single PEST sequence rich in Pro, Glu or Asp, Ser and Thr. It
 CC is expressed significantly in fetal liver and in resting lymphoid cells.
 CC Lyp2 is an isoform of the Lyp1 gene that arises by alternative splicing
 CC of the mRNA. The intronic sequence of Lyp1 encodes for the C-terminal 7
 CC aminoacids and part of the 3' untranslated region of Lyp2. Lyp2 shares
 CC sequence identity with the murine phosphatase Z702EP. Lyp proteins are
 CC important for regulation of T cell antigen and cytokine receptor
 CC signaling and for early and late stages of T cell differentiation. Lyp2
 CC has immunosuppressive activity. Compounds that increase expression of Lyp
 CC protein can be used as immunosuppressive agents to reduce or prevent T
 CC cell activation or proliferation, to control thymocyte differentiation,
 CC to treat autoimmune diseases and transplant situations
 XX
 SQ Sequence 692 AA;
 Query Match 29.2%; Score 708; DB 2; Length 692;
 Best Local Similarity 46.7%; Pred. NO. 5e-58;
 Matches 136; Conservative 54; Mismatches 95; Indels 6; Gaps 4;
 QY 27 AGEFSDIOACSAWADGVCSTVAGSRPENVKRYKDVLPDQTRVLSLQEGHSDY 86
 DB 25 ANEFLKLRQSTKYKADKTYPTVAENAKNKQNKDILPDYSRVLSLITDESSY 84
 QY 87 INGNIRGVGSLAYIATQGPLHTLLDFWRLVWFEFGVKVILMACREIENGKRCERYWA 146
 DB 85 INANIKGVYGPKAYIATQGPLSTLLDFWRLVWFEFGVKVILMACREIENGKRCERYWA 144
 QY 147 QSQE-PLQTGLFCITLKEKLNEDIMLRTLVKTFQKESRSVYQLQVMSWPDGVPSPD 205
 DB 145 EPGEMQLBFGPFSVSCAEK-RKSDYIIRTLKVKFNSETRTIYQHYKNWPDHVPSSID 203
 QY 206 HMLAMVEARLRQGGSPPLCVHCSAGCGRTGLCT-VDYVRQLLITOMIPDFSLFDVW 264
 DB 204 PILELIWVRCVQEDSDVPICHCAGCGRTGVICAIVDYTWMLLKDGIIENFSVSLI 263
 QY 265 LKVRKQRPAAVQTEEQYRFLYHTVAQMF---CSTLQNASPHYQNTKENCAP 312
 DB 264 REMRTQRPVSLVQSQYELVYNVAVLELFPKQMDVIRDKHSGTGSQAKHCIP 314
 RESULT 13
 AAM51205
 ID AAM51205 standard; protein; 780 AA.
 XX
 AC AAM51205;
 XX
 DT 19-DEC-2001 (first entry)
 XX
 DE Human PTP-PEST Gerbank Accession Number XP034191.
 XX
 KW PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
 KW dephosphorylation; phosphotyrosine; human; PTP-PEST.
 XX
 OS Homo sapiens.
 XX
 PN WO200161031-A2.
 XX 23-AUG-2001.
 XX 13-FEB-2001; 2001WO-US005180.
 XX 14-FEB-2000; 2000US-0181769P.
 XX (CEPT-) CEPTYR INC.
 XX Flint AJ, Cool DE;
 XX WPI; 2001-570570/64.
 XX
 PT Screening assays to identify agents that alter protein tyrosine
 PT phosphatase (PTP) binding to, and PTP-mediated catalytic
 PT dephosphorylation of phosphotyrosine peptide substrates.
 XX
 PS Example 1; Page; 79pp; English.
 XX
 CC The invention relates to identifying agents which alter the interaction
 CC between a protein tyrosine phosphatase (PTP) and a tyrosine
 CC phosphorylated polypeptide using fluorescence energy signals. The methods
 CC are useful for performing screening assay to identify agents that alter
 CC PTP binding to and PTP-mediated catalytic dephosphorylation of
 CC phosphotyrosine peptide substrates. The present sequence is not given in
 CC the specification but is that of human PTP-PEST protein sequence taken
 CC from Genbank (Accession Number; XP034191). The present sequence was used
 CC to generate mutants D199A (AAM51201) and C231S (AAM51202) as described in
 CC the specification. Note: An alternative sequence for human PTP-PEST is
 CC given in figure 1 of the specification (AAG78281)
 XX
 SQ Sequence 780 AA;
 Query Match 29.2%; Score 708; DB 4; Length 780;
 Best Local Similarity 40.7%; Pred. NO. 5.9e-58;
 Matches 143; Conservative 66; Mismatches 116; Indels 26; Gaps 7;
 QY 9 RSFLERLEA-----RGREGAVLAGFEFSDIQACSAWADGVCSTVAGSRPENVKRYK 63
 DB 8 RKFIQRVQAMKSPDHNGEDN--FARDFMLRLRLSTKYRTEKIYPTATGKEENVKKNRYK 65
 QY 64 DVLVPTQTRVLSLQEGHSDYINGNIRGVGSLAYIATQGPLHTLLDFWRLVWFEFG 123
 DB 66 DILPFDHRSVKLTKTPSQSDSYINANFIKGVYGPKAYIATQGPLANTVIDFWRMIWEYN 125
 QY 124 VKVILMACREIENGKRCERYW-AQCEPLQTLGFCITLKEKLNEDIMLRTLVKTFQK 182
 DB 126 VTIWVIMACREFEFGKRCERYWPLYGEDPITTFAPFKIS-CEDEQARTDYFIRTLLEFON 184
 QY 183 ESRSVYQLQVMSWPDGVPSPPLCVHCSAGCGRTGLCTV 242
 DB 185 ESRRLIQFHYVNPDPHDVDFSSFDISLMSLRKYQEHEDVPICHCAGCGRTGAICAI 244
 QY 243 DYVRQLLITOMIPDFSLFDVWLMKQKQRPAAVQTEEQYRFLYHTVAQMFCSLQNASPH 302
 DB 245 DYTWMLLKAGKIPEEFNVFNLIQEMRTQKHSVQTEKEQVELVHRAIAQLFQKQLYIEIH 304
 QY 303 YQNIKENCAPLYDDALFLATPQALLAI-----PRPFGVLRISIVPG 344
 DB 305 -----GAQKIADGVNEINTENVMSIEPEKQDSPPPKPPR--TRSLVEG 347
 RESULT 14
 AAY28652
 ID AAY28652 standard; protein; 808 AA.
 XX
 AC AAY28652;
 XX
 DT 01-OCT-1999 (first entry)
 XX
 DE Human Cytoplasmic phosphatase, Lyp1 protein.
 XX

Lymphoid Protein Tyrosine Phosphatase; Lyp protein; lymphoid cell; intracellular tyrosine phosphatase; PTPase; lymphocyte; thymocyte; T cell; B cell; protein tyrosine kinase; PKs; immunosuppressant; T cell antigen receptor signalling; cytokine receptor signalling; autoimmune disease; transplant.

OS Homo sapiens.

Key Location/Qualifiers

Domain 27..289 /label= pTPase_domain /note= "Single catalytic protein tyrosine phosphatase domain"

Domain 469..472 /label= NXXY_motif /note= "Unique sequence recognised by phosphotyrosine binding (PTB) domain"

Binding-site 615..623 /label= SH3 binding site /note= "Proline rich sequence"

Binding-site 694..701 /label= SH3 binding site /note= "Proline rich sequence"

Region 702..736 /label= SH3 binding site /note= "Proline rich sequence"

Region 741..745 /label= PEST sequence /note= "Sequence rich in Pro, Glu or Asp, Ser and Thr"

Binding-site 768..772 /label= SH3 binding site /note= "Consensus sequence recognised by p34cdc2 kinase"

Binding-site 796..804 /label= SH3 binding site /note= "Proline rich sequence"

Binding-site /label= SH3 binding site /note= "Proline rich sequence"

XX WO9936548-A1.

XX 22-JUL-1999.

XX 18-JAN-1999; 99WO-CA000038.

XX 16-JAN-1998; 98CA-02220853.

XX (HSCR-) HSC RES & DEV LP.

XX Roifman CM;

XX WPI; 1999-444404/37.

XX N-PSDB; AAX90695.

XX New nucleic acid encoding intracellular tyrosine phosphatase and related proteins, used to modulate signaling through T cells, particularly as immunosuppressant.

PS Claim 4a; Page 53; 105pp; English.

XX The present protein sequence is that of the cytoplasmic, Lymphoid Protein Tyrosine Phosphatase Lyp1, that has a single catalytic domain. The non-catalytic portion of the phosphatase contains unique sequences, including a single PEST sequence rich in Pro, Glu or Asp, Ser and Thr. Lyp1 is expressed in the lymphoid cells, particularly in thymocytes, mature B and T cells and expression is increased upon activation. It is involved in lymphocyte growth and development and is phosphorylated in a cell cycle dependent manner. Lyp1 shares about 70% sequence identity with the murine phosphatase 270BP. Lyp proteins are important for regulation of T cell antigen and cytokine receptor signalling and for early and late stages of T cell differentiation. Lyp1 has immunosuppressive activity. Compounds that increase expression of Lyp protein can be used as immunosuppressive agents to reduce or prevent T cell activation or proliferation, to control thymocyte differentiation and to treat autoimmune diseases and transplant situations

XX Sequence 808 AA;

Query Match 29.2%; Score 708; DB 2; Length 808;
Best Local Similarity 46.7%; Pred. No. 6.2e-58;

Matches 136; Conservative 54; Mismatches 95; Indels 6; Gaps 4;

QY 27 AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKRYKQVLFDQTRVILSLQEGHSDY 86

DB 25 ANEFLKLRQSTKYKADKTYPTTVAENAKNKKRYKQILPYDSRVLSLITSDSSY 84

QY 87 INGNFIRGVDGLAYIATQGPLHTLLDFWRLVWFEFGVKVILMACREIENGKRCERYWA 146

DB 85 INANFIKGVYGPXAYIATQGPLSTLLDFWRLVWFEFGVKVILMACREIENGKRCERYWA 144

QY 147 QSQE-PLQTGLFCITLKEKWLNEDIMLTLLKVTQKSSRSVYQYMSWDRGVPSSPD 205

DB 145 EPGEMQLEFGPPFSVCEAEK-RKSDYIITLKVENSETRTIYQHYQWPDHVPSSID 203

QY 206 HMLAMVEEARLQGGSPPELCVHCSAGCGRTGVLCT-VDYVRQLLLTQMIPDFSLFDVW 264

DB 204 PILELIWVRCVQEDDSVPICHCAGCGRTGVI-CAIVDTYMWLLKDGIIENFSVFSLI 263

QY 265 LKVRKQRPAAVQTEBQYRFLYHTVQMF---CSTLQNASPHYQNTKENCAP 312

DB 264 REMRTQRPSTVQEQYELVYNAVLELFRQMDVIRDKHSGTESQAKHCIP 314

RESULT 15

AA567250

ID AAY67250 standard; protein; 775 AA.

XX AAY67250;

DT 05-APR-2000 (first entry)

DE Mouse protein tyrosine phosphatase (PTP) PEST amino acid sequence.

XX Protein tyrosine phosphatase; PTP; PEST; paxillin binding; adhesion;

KW cell migration; division; cytostatic; antiinflammatory; angiogenesis;

KW cancer; enzyme substrate identification; mouse.

XX Mus sp.

XX Key Location/Qualifiers

FT Domain 332..339

FT /label= Pro 1

FT /note= "Proline rich domain 1"

FT Domain 355..364

FT /label= Pro 2

FT /note= "Proline rich domain 2"

FT Domain 519..528

FT /label= Pro 3

FT /note= "Proline rich domain 3"

FT Domain 675..681

FT /label= Pro 4

FT /note= "Proline rich domain 4"

FT Domain 764..771

FT /label= Pro 5

FT /note= "Proline rich domain 5"

XX WO9961467-A2.

XX 02-DEC-1999.

XX 21-MAY-1999; 99WO-CA0000461.

XX 21-MAY-1998; 98CA-02238654.

XX 11-DEC-1998; 98US-0111993P.

XX (UYMC-) UNIV MCGILL.

XX Tremblay ML, Cote J, Angers-Lousteau A, Charest A;

XX WPI; 2000-097104/08.

DR

XX Novel therapeutic agents for treating diseases which are related to cell
PT proliferation, migration, inflammation and angiogenesis especially
PT cancer.
XX
PS Claim 4; Fig 24; 91pp; English.
XX
CC This is the amino acid sequence of mouse protein tyrosine phosphatase
CC (PTP). PTP-PEST is a soluble PTP that is ubiquitously expressed
CC throughout embryonic development and in murine adult tissues. The N-
CC terminal portion of the enzyme encodes for the catalytic domain, while
CC the C-terminal portion is composed of 5 proline rich domains, and a
CC binding site for the adaptor protein Shc. The pro 2 domain is required
CC for paxillin binding, and the synthesis of mutant PTP-PEST have shown
CC that proline 362 is important for paxillin binding activity. The
CC invention relates to a compound that is capable of interfering with the
CC binding of PTP-PEST to signalling molecules that are involved in cell
CC migration, adhesion or division. The compound can be derived from minimal
CC sequences found in binding sites of PTP-PEST. The invention also relates
CC to a method for finding a genuine substrate for an enzyme in a cell that
CC normally expresses the wild type form of the enzyme. A mutant version of
CC PTP-PEST (see AY67251 and AY67253) is used in this method. The
CC compounds have cytostatic and antiinflammatory activity. The compounds
CC are used for making medicaments for treating a disease related with cell
CC proliferation, migration, inflammation and angiogenesis, especially
CC cancer. The novel method is used for identifying a genuine substrate for
CC an enzyme
XX
SQ Sequence 775 AA;
Query Match 29.1%; Score 705; DB 3; Length 775;
Best Local Similarity 25.0%; Pred. No. 1.1e-57;
Matches 194; Conservative 84; Mismatches 162; Indels 336; Gaps 17;
QY 9 RSFLERLEA-----RGGREGAVLAGESDIOACSAANKADGVCSTVAGSPENVRKNRYK 63
DB 8 RRFQVQAMKSPDHNEEDN--FARDFWRLRLTKYRTEKIYPTATGEKEENVKKNRYK 65
QY 64 DVLPTDQTRVILSLQEEHSDYINGNFIKGVGSLAYIATQGPPLHTLDFWRLVWFEFG 123
DB 66 DILFFDHSRVKLTLPKTSQDSYINANFIKGVYKAVVATQGPFRNTVIDFWRMIWEYN 125
QY 124 KVVILMACRETEKRCERYW--KQEQEPLQTGLFCITLKEKWLNEIDMLRTLKVTFOK 182
DB 126 VVIIVMACREFEMGKCKERYWPLYGEDPITFAPFKISCENEQ--ARTDYFIRTLLEFON 184
QY 183 ERSVYQLQYMSWDRGVPSPDHMLAMVEARLQSGPPEPLCVHCSAGCGRTGVLCTV 242
DB 185 ESRRLYQFHYVNNPDHVPSSFDILDMI SLMRKYQHEDVPICHCSAGCGRTGAICAI 244
QY 243 DYVRQLLLTOMIPDFSLFDVVLKMRKQRPAAVQTESQYRFLYHTVAQMFCSTLQ----- 297
DB 245 DYTWNLLKAGKIPBEFNFVNLQEMRTQRHSAVQTKQYELVHRAIAQLFEKQLQLYEIH 304
QY 298 ----- 297
DB 305 GAQKIADGNEITTTGTMVSSIDSEKQSGPPPKPPTRSCLVEGDAKEIILQPPPEHPVPI 364
QY 298 -----NASP----- 301
DB 365 LTPSPSAPFTVTTWQSDRYHPKPVHLHMASPQHPADLNRSYDKSQDWKGSESAIEH 424
QY 302 -----HYQNIKENCAPLYDDALFLRT--POA 325
DB 425 IDKKLERLNSPEIKVPLQEGFKGFDGNTLLNRGHAIKIKSASSSVVD-----RTSRPQE 479
QY 326 LLA-----IPRP-----PGGLRSI- 340
DB 480 LSAGALKYDDVYQNSCADCSAAHSHRAESSEESQNSHTPPRDCPLDKKGHTVWSLH 539
QY 341 -----SVPGSPGHAMADTY-----ABEQKR----- 360
DB 540 GPNATPVDPSPDGKSPNHSQTLKTVSTPNSTAEAEHADLTEHNSPILLKAPLSFTN 599

QY 361 -----CAPAGASGTGTGTGTCG-----RSAEAPLYSKVTPR----- 393
DB 600 PLHSDDWHSDDGSGDGAIVTRNKTSTISATVSPASSAESACHRRVLEPMSIARQEVAGTP 659
QY 394 ---AQRPGAHADARGTLPGRVP----- 413
DB 660 HSGAEKDADVSESPPLPERTFESFVLADMPVRPEWHELPNQEWSEQSESEGLTTSUNE 719
QY 414 -----ADOSPAGSGAYEDVA--GGAQTGGGLGNLAIGRKGPDRDPAEWNT 456
DB 720 KHDAGGIHTASADSPPAFSDKKDQITKSPAIEVTDIGFGNRCGKPKGPREPPESEWT 775

Search completed: August 17, 2004, 20:42:49
JOB time : 56 secs

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